



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109990

**TO: Lorraine Spector
Location: CM-1/10B11/10B19
Art Unit: 1647
Tuesday, December 09, 2003**

Case Serial Number: 09/996569

**From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203**

edward.hart@uspto.gov

Search Notes

Examiner Spector,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

From: Hutzell, Paula
Sent: Monday, December 08, 2003 4:01 PM
To: Spector, Lorraine; STIC-Biotech/ChemLib
Subject: RE: 09/996569

approved

-----Original Message-----

From: Spector, Lorraine
Sent: Monday, December 08, 2003 3:53 PM
To: Hutzell, Paula
Subject: FW: 09/996569

Paula,
would you please authorize this as a rush search? Reasons evident.
Thanks,
Lori

-----Original Message-----

From: Hanley, Susan
Sent: Monday, December 08, 2003 3:51 PM
To: Spector, Lorraine
Subject: RE: 09/996569

*I'm afraid that I can't help you out with this request. As of last week, I rejoined the patent examining corps. If you want more alignments, you will have to request a new search. The standard search set-up provides 15 alignments and that's it.
The searcher cannot print out more alignments because the computer only posted 15 of the results to be displayed with alignments.
Protein searches should turn around in 2 days max.*

*Susan Hanley
US Patent and Trademark Office
Art Unit 1651
Office: 11E07 Mail Box: 11B01
Phone: 703-305-1982*

-----Original Message-----

From: Spector, Lorraine
Sent: Monday, December 08, 2003 3:41 PM
To: Hanley, Susan
Subject: 09/996569

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 12/9/03
Date Completed: 12/9/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: QSP
WWW/Internet: _____
Other (specify): _____

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

Importance: High

Susan,

You ran a search for me on this case on 11/26, on sequence ID NO:2

Could you please print out more hits for the oligo search in the .rag and .rai databases only?

I'd like to see all hits down to 10 contiguous residues.

Thanks,

Lori

Lorraine Spector, Ph.D.

Patent Examiner

U.S. Patent and Trademark Office

CM1, 10B-11

703-308-1793

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library GM1 - Circ. Desk



GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:44:40 ; Search time 47 seconds
(without alignments)
1827.044 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSLHVMGLGSL.....DDLMEKSPRPMSNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	AAW12695	G-protein parathyr
2	363	67.1	550	AAW1875	Human PTH seven t
3	363	67.1	550	ABUS5732	Lung cancer-associ
4	363	67.1	550	ABP81871	Human parathyroid
5	342	63.2	561	ABUS56731	Lung cancer-associ
6	262	48.4	550	ABBS56386	Non-endogenous hum
7	262	48.4	550	AAW80560	Human PTH2 recepto
8	38	7.0	546	AAW80559	Rat PTH2 receptor
9	25	4.6	515	AAW27704	Opussum kidney PTH

10	25	4.6	515	17	AAW92275	Opussum kidney PTH
11	25	4.6	515	20	AAW73314	Parathyroid hormon
12	25	4.6	585	13	AAW27705	Opussum kidney PTH
13	25	4.6	585	17	AAW92276	Opussum kidney PTH
14	25	4.6	585	20	AAW73315	Parathyroid hormon
15	22	4.1	864	22	ABG27219	Novel human diago
16	20	3.7	20	24	ABP82552	G protein-coupled
17	19	3.5	440	21	AAW80188	Amino acid sequenc
18	19	3.5	440	22	ABBS56387	Non-endogenous hum
19	19	3.5	440	22	AAW71877	Human SCRC seven t
20	19	3.5	440	23	ABW8012	Protein identified
21	19	3.5	440	23	ABBS1202	Human secretin rec
22	19	3.5	440	24	ABP81912	Human secretin rec
23	19	3.5	449	13	AAW30187	Secretin receptor.
24	18	3.3	18	24	ABP82551	G protein-coupled
25	18	3.3	324	21	AAW96985	Tethered PTH-1 rec
26	18	3.3	335	21	AAW96984	Tethered PTH-1 rec
27	18	3.3	435	21	AAW96987	Human tethered PTH
28	18	3.3	435	21	AAW07529	A mutant parathyro
29	18	3.3	446	21	AAW96983	Tethered PTH-1 rec
30	18	3.3	448	21	AAW96986	Human tethered PTH
31	18	3.3	450	21	AAW96988	Human tethered PTH
32	18	3.3	536	21	AAW99600	Zebrafish parathyr
33	18	3.3	536	21	AAW90230	Zebrafish PTHrP re
34	18	3.3	591	13	AAW27706	Rat bone PTH/PTHrP
35	18	3.3	591	17	AAW92277	Rat bone PTH/PTHrP
36	18	3.3	591	20	AAW73316	Parathyroid hormon
37	18	3.3	593	17	AAW92278	Human kidney PTH/P
38	18	3.3	593	20	AAW73317	Human Parathyroid
39	18	3.3	593	22	ABBS56385	Non-endogenous hum
40	18	3.3	593	22	AAW71876	Human PTHrP seven t
41	18	3.3	593	24	ABP81872	Human parathyroid
42	18	3.3	595	24	ABG73825	Canine parathyroid
43	18	3.3	614	13	AAW27707	Human kidney PTH/P
44	16	3.0	447	23	ABW79169	Carassius auratus
45	14	2.6	19	13	AAW27710	PTH/PTHrP receptor

ALIGNMENTS

RESULT 1

AAW12695
ID AAW12695 standard; Protein; 541 AA.

XX AC AAW12695;

XX DT 31-MAY-1997 (first entry)

XX XX G-protein parathyroid hormone receptor HLTG74.

DE G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH.

XX KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;

XX KW hyperphosphataemia; hypoparathyroidism; chronic tetany;

XX KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;

XX KW kidney stone; nephrolithiasis; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WO9639433-A1.

XX XX 12-DEC-1996.

XX PF 05-JUN-1995; 95WO-US07085.

XX PR 05-JUN-1995; 95WO-US07085.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX WPI; 1997-043068/04.

XX DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
PS
XX Claim 9; Fig 1A-E; 62pp; English.
XX
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AA159619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephrolisis.
XX
SQ Sequence 541 AA;

Query Match 100.0%; Score 541; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLHVGWMLGSCCLLARAQLDSGTTIEBQIVLVKAKVQCELNITAOQEGR 60
Db 1 MAWLGLSLHVGWMLGSCCLLARAQLDSGTTIEBQIVLVKAKVQCELNITAOQEGR 60

QY 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFHSLNKTWA 120
Db 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFHSLNKTWA 120

QY 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIIIGYFRLHCTERNYIH 180
Db 121 NYSDCRLFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAIIIGYFRLHCTERNYIH 180

QY 181 MHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQSYIGCKIAV 240
Db 181 MHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQSYIGCKIAV 240

QY 241 VMFIYLATNYWMLVEGLYHNLIFVAFPSDTKYLWGFTLIGWGFPAFVAWAVARAT 300
Db 241 VMFIYLATNYWMLVEGLYHNLIFVAFPSDTKYLWGFTLIGWGFPAFVAWAVARAT 300

QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFIPLNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFIPLNTVRVLATKIWETNAVGHDTKQYRK 360

QY 361 LAKSTLVLVLRGVHYIVFVCLPHSFTGLGWEIRMECELPFNSFOGFFVSIYCYNGEV 420
Db 361 LAKSTLVLVLRGVHYIVFVCLPHSFTGLGWEIRMECELPFNSFOGFFVSIYCYNGEV 420

QY 421 QAEVKKWRNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
Db 421 QAEVKKWRNLSVDWKRTPPCGSRRCGSVLTTVTHSTSSQSVAAAHAWCLSLAKLPR 480

QY 481 SPADSLTATSLYLANGVTSQRTASHTLSTRNKEDSGRQDDILMEKSPRPMESNPDE 540
Db 481 SPADSLTATSLYLANGVTSQRTASHTLSTRNKEDSGRQDDILMEKSPRPMESNPDE 540

QY 541 G 541
Db 541 G 541

RESULT 2
AAB71875
ID AAB71875 standard; Protein; 550 AA.
XX
AC AAB71875;
XX

DT 03-MAY-2001 (first entry)
XX
DE Human PTR2 seven transmembrane domain.
XX
KW Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
KW graft rejection; cystic fibrosis.
XX
OS Homo sapiens.
XX
PN WO200109328-A1.
XX
PD 08-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-US21278.
XX
PR 03-AUG-1999; 99US-0146916.
XX
PR 29-FEB-2000; 2000US-0515781.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA Hodge MR, Lloyd C, Weich NS;
XX
PI WPI; 2001-138653/14.
XX
DR Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.
XX
PS Disclosure; Fig 2; 145pp; English.
XX
CC The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.
XX
SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 22; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHVWGMGLGSCCLLARAQLDSGTTIEBQIVLVKAKVQCELNITAOQEGRNC 63
Db 4 LGASLHVWGMGLGSCCLLARAQLDSGTTIEBQIVLVKAKVQCELNITAOQEGRNC 63

QY 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFHSLNKTWANS 123
Db 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFHSLNKTWANS 123

QY 124 DCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAIIIGYFRLHCTERNYIHML 183
Db 124 DCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAIIIGYFRLHCTERNYIHML 183

QY 184 FVSFMLRATSIKVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQSYIGCKIAVNF 243
Db 184 FVSFMLRATSIKVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQSYIGCKIAVNF 243

QY	244	IYFLATNYWIIIVGELYIHNLI	FVAF	FDSDTKYLNGFII	GWGFP	PAAFVAAW	VARATLAD	303		
Db	244	IYFLATNYWIIIVGELYIHNLI	FVAF	FDSDTKYLNGFII	GWGFP	PAAFVAAW	VARATLAD	303		
QY	304	ARCWELSGADIKWIIYQAPIL	AAIG	NFII	FLNTVRLV	ATKI	WETNAVGHDT	KQYRKLA	363	
Db	304	ARCWELSGADIKWIIYQAPIL	AAIG	NFII	FLNTVRLV	ATKI	WETNAVGHDT	KQYRKLA	363	
QY	364	STLVLVLFVGVHYIVFVCL	PHSF	TGLGWEIR	MHC	ELF	FNFS	FOGFFVSI	IYCNGEVOAE	423
Db	364	STLVLVLFVGVHYIVFVCL	PHSF	TGLGWEIR	MHC	ELF	FNFS	FOGFFVSI	IYCNGEVOAE	423
QY	424	VKKQWSRWNL	SVDW	WKRT	PPCG	SRRC	GSVLT	TVTH	STSSQSVAA	467
Db	424	VKKQWSRWNL	SVDW	WKRT	PPCG	SRRC	GSVLT	TVTH	STSSQSVAA	467
RESULT	3									
ABU	56732	standard; Protein; 550 AA.								
AC	ABU56732;									
XX	02-APR-2003	(first entry)								
DT	Lung cancer-associated polypeptide #325.									
XX	Lung cancer-associated polypeptide; cytosstatic; emphysema;									
XX	antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;									
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;									
KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;									
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.									
XX	Unidentified.									
OS	Unidentified.									
XX	WO200286443-A2.									
PN	31-OCT-2002.									
XX	18-APR-2002; 2002WO-US12476.									
PF	18-APR-2001; 2001US-284770P.									
XX	10-MAY-2001; 2001US-290492P.									
PR	09-NOV-2001; 2001US-339245P.									
PR	13-NOV-2001; 2001US-350666P.									
PR	29-NOV-2001; 2001US-334370P.									
PR	12-APR-2002; 2002US-372246P.									
XX	(BOSB-) BOS BIOTECHNOLOGY INC.									
XX	PA									

CC	cancer, non-small cell lung cancer or other benign or precancerous
CC	lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC	pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC	pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC	and polypeptides are useful for diagnostic purposes and as targets for
CC	screening for therapeutic compounds that modulate lung cancer, such as
CC	antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC	polypeptides of the invention.
XX	
SQ	Sequence 550 AA;
	Query Match 67.1%; Score 363; DB 24; Length 550;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps
QY	4 LGASHVWGWLMLGSLARQAQLSDGTTTTEEQIVLVLKAKVQCELNITAOIQEGNC 63
DB	4 LGASHVWGWLMLGSLARQAQLSDGTTTTEEQIVLVLKAKVQCELNITAOIQEGNC 63
QY	64 PPEWDGLICWPRGTGKISAVPCPPYIVDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
DB	64 PPEWDGLICWPRGTGKISAVPCPPYIVDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
QY	124 DCLRFLQPDISIGKQEPFERYVMYTVGYGISFGLSAVAILLIGYFRRLHCTRNTHMEL 183
DB	124 DCLRFLQPDISIGKQEPFERYVMYTVGYGISFGLSAVAILLIGYFRRLHCTRNTHMEL 183
QY	184 FVSPMLRATSFVKDRVVAHHGVKELESIMQDDPQNSIEATSDVKSGYIGCKIAVMVF 243
DB	184 FVSPMLRATSFVKDRVVAHHGVKELESIMQDDPQNSIEATSDVKSGYIGCKIAVMVF 243
QY	244 IYFLATNYTWLVEGLYLHNLIVFAFPDSTKYLWGFIILGWGFPAFVAAMAVARATLAD 303
DB	244 IYFLATNYTWLVEGLYLHNLIVFAFPDSTKYLWGFIILGWGFPAFVAAMAVARATLAD 303
QY	304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLA 363
DB	304 ARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLA 363
QY	364 STLVLVLVFGVHYIVFVCLPHSFFTGLGWEIRHMCLELFPNSFGPFVSIYYCNGEVQAE 423
DB	364 STLVLVLVFGVHYIVFVCLPHSFFTGLGWEIRHMCLELFPNSFGPFVSIYYCNGEVQAE 423
QY	424 VKKWSRNLSVDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAA 467
DB	424 VKKWSRNLSVDWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAA 467
RESULT 4	
ABP81871	
ID	ABP81871 standard; Protein; 550 AA.
AC	ABP81871;
DT	04-MAR-2003 (first entry)
DE	Human parathyroid hormone receptor 2 protein SEQ ID NO:227.
KW	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW	G protein-coupled receptor modulator; antibody; immune-related disease;
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW	immunological-related cell proliferative disease; autoimmune disease;
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
OS	Homo sapiens.
XX	
FN	WO200261087-A2.

XX PD 08-AUG-2002.
XX PF 19-DEC-2001; 2001WO-US50107.
XX PR 19-DEC-2000; 2000US-257144P.
XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX PI Burner GC, Roush CL, Brown JP;
XX PR WPI; 2003-046718/04.
XX DR N-PSDB; AB242718.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases -
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising:
XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related diseases, cell diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.
XX
XX Sequence 550 AA;
XX
XX Query Match 67.1%; Score 363; DB 24; Length 550;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4 LGASHVWGMMLGSLILARAQLSDGTTTIEQIVLVILKAKVQCELNITAIQLEGNC 63
XX Db 4 LGASHVWGMMLGSLILARAQLSDGTTTIEQIVLVILKAKVQCELNITAIQLEGNC 63
XX
XX QY 64 FPEWGLICPRGTGKISAVCPPIYDFNKHGVAFRHCNPNGTWDFMHSINKTWANYS 123
XX Db 64 FPEWGLICPRGTGKISAVCPPIYDFNKHGVAFRHCNPNGTWDFMHSINKTWANYS 123
XX
XX QY 124 DCLFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIHML 183
XX Db 124 DCLFLQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIHML 183
XX
XX QY 184 FYSEMLRATSIYKDRVVAHIGVKELESILNQDDPQNSIATSDVKQYIGCKIAVMVF 243
XX Db 184 FYSEMLRATSIYKDRVVAHIGVKELESILNQDDPQNSIATSDVKQYIGCKIAVMVF 243
XX
XX QY 244 IYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAFAVAWAVARATLAD 303
XX Db 244 IYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAFAVAWAVARATLAD 303
XX
XX QY 304 ARCWELSGDIKWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 363
XX Db 304 ARCWELSGDIKWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAK 363
XX
XX QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCFLFNSFGQFFVSIYCYCNSEVQAB 423
XX Db 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCFLFNSFGQFFVSIYCYCNSEVQAB 423
XX
XX QY 424 VKKMSRWNLSDWKRTPPCGSRRRCGSLTITVTHSTSSQSQVAA 467
XX Db 424 VKKMSRWNLSDWKRTPPCGSRRRCGSLTITVTHSTSSQSQVAA 467
XX
XX RESULT 5
XX ABU56731
XX ID ABU56731 standard; Protein; 561 AA.
XX AC ABU56731;
XX
XX DT 02-APR-2003 (first entry)
XX
XX DE Lung cancer-associated polypeptide #324.
XX
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema; antinflammatory; antiasthmatic; non-small cell lung cancer; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
XX OS Unidentified.
XX
XX XX WO200286443-A2.
XX PD 31-OCT-2002.
XX
XX PF 18-APR-2002; 2002WO-US12476.
XX
XX PR 18-APR-2001; 2001US-284770P.
XX PR 10-MAY-2001; 2001US-290492P.
XX PR 09-NOV-2001; 2001US-339245P.
XX PR 13-NOV-2001; 2001US-350666P.
XX PR 29-NOV-2001; 2001US-334370P.
XX PR 12-APR-2002; 2002US-372246P.
XX
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX PI Aziz N, Murray R;
XX
XX DR WPI; 2003-093161/08.
XX DR N-PSDB; ABX76460.
XX
XX PT Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer -
XX
XX PS Claim 27; Page 439; 453pp; English.
XX
XX CC The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides

CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
 CC polypeptides of the invention.

XX SQ Sequence 561 AA;
 Query Match 63.2%; Score 342; DB 24; Length 561;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 25 QLDSDGTITIEQIVLVKAKVQCELNITAIQOEGEGNCFPWDGLICWPRGTGKISAV 84
 DB 36 QLDSDGTITIEQIVLVKAKVQCELNITAIQOEGEGNCFPWDGLICWPRGTGKISAV 95
 QY 85 PCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANTSDCLRFLOPDISIGKQFCRRL 144
 DB 96 PCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANTSDCLRFLOPDISIGKQFCRRL 155
 QY 145 YMYTVGYISFGSLAVAILIIGYFRLHCTRNYYIMHILFVSGFMLRATSIYFKDRVVAH 204
 DB 156 YMYTVGYISFGSLAVAILIIGYFRLHCTRNYYIMHILFVSGFMLRATSIYFKDRVVAH 215
 QY 205 IGKLESLIMODDPQNSIEATSDKSOYIGCKIAVWPIYFLATNYWILVEGLYIHNIL 264
 DB 216 IGKLESLIMODDPQNSIEATSDKSOYIGCKIAVWPIYFLATNYWILVEGLYIHNIL 275
 QY 265 IFVAFPSDTKYLWGFLILGWGPPAFAVAWAVARATLADARCWELSGDIKIWIQAPILA 324
 DB 276 IFVAFPSDTKYLWGFLILGWGPPAFAVAWAVARATLADARCWELSGDIKIWIQAPILA 335
 QY 325 AIGLNILFINTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVFGVHHYIVFVCLPH 384
 DB 336 AIGLNILFINTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVFGVHHYIVFVCLPH 395
 QY 385 SFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAEVKKWWSRWNLSDWKRTPPCG 444
 DB 396 SFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAEVKKWWSRWNLSDWKRTPPCG 455
 QY 445 SRRCGSVLTVTHTSTSSQSVAA 467
 DB 456 SRRCGSVLTVTHTSTSSQSVAA 478

RESULT 6
 ABB56386
 ID ABB56386 standard; Protein; 550 AA.
 AC ABB56386;
 XX ABB56386;
 DT 18-FEB-2002 (first entry)
 XX Non-endogenous human GPCR protein, SEQ ID NO: 565.
 DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.

XX Homo sapiens.
 OS Synthetic.
 XX WO200177172-A2.
 XX 18-OCT-2001.
 XX 05-APR-2001; 2001WO-US11098.
 XX 07-APR-2000; 2000US-195747P.
 XX (AREN-) ARENA PHARM INC.
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 PI WPI; 2001-648759/74.

DR N-PSDB; AB198022.
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -
 XX Claim 1; Page 367-369; 394pp; English.
 XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.

XX SQ Sequence 550 AA;

Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LGASLHVWGMILGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAIQOEGEGNC 63
 DB 4 LGASLHVWGMILGSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAIQOEGEGNC 63
 QY 64 FPWMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANTYS 123
 DB 64 FPWMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWANTYS 123
 QY 124 DCLRFLOPDISIGKQFCRRLYMYTVGYISFGSLAVAILIIGYFRLHCTRNYYIMHIL 183
 DB 124 DCLRFLOPDISIGKQFCRRLYMYTVGYISFGSLAVAILIIGYFRLHCTRNYYIMHIL 183
 QY 184 FVSGFMLRATSIYFKDRVVAHIGKLESLIMODDPQNSIEATSDKSOYIGCKIAVWVF 243
 DB 184 FVSGFMLRATSIYFKDRVVAHIGKLESLIMODDPQNSIEATSDKSOYIGCKIAVWVF 243
 QY 244 IYFLATNYWILVEGLYIHNILIFVAFPSDTKYLWGFLILGWGPPAFAVAWAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYIHNILIFVAFPSDTKYLWGFLILGWGPPAFAVAWAVARATLAD 303
 QY 304 ARCWELSGDIKIWIQAPILAAIGLNILFINTVRLATKIWETNAVGHDTKQYRKLAK 363
 DB 304 ARCWELSGDIKIWIQAPILAAIGLNILFINTVRLATKIWETNAVGHDTKQYRKLAK 363
 QY 364 STLVLVFGVHHYIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAE 423
 DB 364 SPLVLVFGVHHYIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSIYCYCNGEVOAE 423
 QY 424 VKKWSRWNLSDWKRTPPCGSRRCSVLTVTHTSTSSQSVAA 467
 DB 424 VKKWSRWNLSDWKRTPPCGSRRCSVLTVTHTSTSSQSVAA 467

RESULT 7
 AAB80560
 ID AAB80560 standard; Protein; 550 AA.
 AC AAB80560;
 XX AAB80560;
 DT 26-APR-2001 (first entry)
 XX Human PTH2 receptor amino acid sequence.
 DE Tuberinfundibular peptide of 39 residues; TIR39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimitotic; antidiabetic; osteopathic; hypertensive; cardiac;
 KW cytosolic; antisthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;

KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Homo sapiens.
 XX WO200077042-A2.
 PN 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 PF 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 DR New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig I; 106pp; English.
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiatic, cyostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX Sequence 550 AA;
 Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LGASLHVWGMVLMGSCLLARAQLDSGTITIEBQIVLVKAKVQCELNITAOIQEGEGNC 63
 DB 4 LGASLHVWGMVLMGSCLLARAQLDSGTITIEBQIVLVKAKVQCELNITAOIQEGEGNC 63
 QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRCPNGTWDFMHSLNKTWANTS 123
 DB 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRCPNGTWDFMHSLNKTWANTS 123
 QY 124 DCLRFLOPDISIGKQFCERLYWYTVGYSISFGSLAVAILIIGYPRRLHCTRNTHMEL 183
 DB 124 DCLRFLOPDISIGKQFCERLYWYTVGYSISFGSLAVAILIIGYPRRLHCTRNTHMEL 183
 QY 184 FVSFMLRATSIKVKDRVVAHIGVKELESIMODDPNSIATSVDSKSVIGCKIAVVMF 243
 DB 184 FVSFMLRATSIKVKDRVVAHIGVKELESIMODDPNSIATSVDSKSVIGCKIAVVMF 243
 QY 244 IYFLATNYWILVEGLYHLNLIYFAFFSDTKYLMGFIILGWGFPFAFVAAMAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYHLNLIYFAFFSDTKYLMGFIILGWGFPFAFVAAMAVARATLAD 303
 QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTTRKQYKLA 363

DB 304 ARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTTRKQYKLA 363
 QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEVOAE 423
 DB 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEVOAE 423
 QY 424 VKKMSRNWLSVDMKRTTPCGSRRCGSVLTTHSTSSQSQVAA 467
 DB 424 VKKMSRNWLSVDMKRTTPCGSRRCGSVLTTHSTSSQSQVAA 467
 RESULT 8
 AAB80559
 ID AAB80559 standard; Protein; 546 AA.
 XX AAB80559;
 XX 26-APR-2001 (first entry)
 XX Rat PTH2 receptor amino acid sequence.
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;
 KW cyostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Rattus sp.
 XX WO200077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 XX treating e.g. migraine or headaches, hypertension, obesity and other
 XX eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig I; 106pp; English.
 CC The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiatic, cyostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX

SQ Sequence 546 AA;

Query Match 7.0%; Score 38; DB 22; Length 546;
Best Local Similarity 100.0%; Pred. No. 8.5e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHD 353
|||||
Db 313 WIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHD 350
|||||

RESULT 9

AAAR27704

ID AAR27704 standard; Protein; 515 AA.

XX

AC AAR27704;

XX

25-MAR-2003 (updated)

DT 16-MAR-1993 (first entry)

XX

DE Opossum kidney PTH/PTHrP receptor prep. from clone OK-H.

XX

KW Parathyroid hormone; related protein; calcium; antagonist;

KW antibodies; hypercalcaemia.

XX

OS Didelphis virginiana.

XX

FN WO9217602-A1.

XX

PD 15-OCT-1992.

XX

06-APR-1992; 92WO-US02821.

XX

05-APR-1991; 91US-0681702.

PR

06-APR-1992; 92US-0864475.

XX

(GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX

PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;

PI Segre GV;

XX

N-PSDB; AAQ29604.

XX

PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
- for (differential) diagnosis of hypercalcaemia, and diagnosis
and treatment of tumours

PT

XX

PS Disclosure; Fig 1; 91pp; English.

XX

CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
receptor protein sequence was deduced from the DNA sequence of the
clone OK-H, isolated from opossum kidney (OK) cells. The protein
may be used in a therapeutic compsn. to inhibit activation of PTH or
PTHrP and thus reduce the level of calcium in the blood. Cpsd.
capable of competing with PTH or PTHrP for binding can be identified
using the protein prod. and DNAs homologous to PTH DNA can be
identified using fragments of the clone as probes. The protein
may be used for the prodn. of antibodies useful for the treatment,
classification, prognosis and/or treatment of disorders related to
the interaction between a cell receptor and a ligand such as in
hypercalcaemia. See also AAR27703-16.
(Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 515 AA;

Query Match

Best Local Similarity 4.6%; Score 25; DB 13; Length 515;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191

|||||

Db 207 GYFRLHCTRNTHMHLFVSFMLRA 231

RESULT 10

AAAR92275

ID AAR92275 standard; Protein; 515 AA.

XX

AC AAR92275;

XX

25-MAR-2003 (updated)

DT 18-MAY-1996 (first entry)

XX

DE Opossum kidney PTH/PTHrP receptor.

XX

KW Parathyroid hormone; receptor; parathormone; PTH;
parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
hypercalcaemia; hypocalcaemia; cancer; opossum.

KW

OS Didelphis virginiana.

XX

FN US5494806-A.

XX

27-FEB-1996.

XX

06-APR-1992; 92US-0864475.

XX

06-APR-1992; 92US-0864475.

PR

05-APR-1991; 91US-0681702.

XX

(GEHO) GEN HOSPITAL CORP.

XX

PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT,

PI Schipani E, Segre GV;

XX

WPI; 1996-139028/14.

XX

N-PSDB; AAT15945.

XX

PT DNA encoding vertebrate parathyroid hormone receptor - useful for

PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,

PT cancer etc.

XX

PS Claim 1; Fig 1A-1E; 64pp; English.

XX

CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
(AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
separate genes or of a laboratory artifact. The receptor induces an
increase in intracellular cAMP and calcium when challenged with PTH or
PTHrP. Recombinant receptors can be produced in vector/host cell systems
and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
Host cells expressing the receptor can be used for diagnostic
measurement of PTH serum levels.
(Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 515 AA;

Query Match

Best Local Similarity 4.6%; Score 25; DB 17; Length 515;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191

|||||

Db 207 GYFRLHCTRNTHMHLFVSFMLRA 231

RESULT 11

AAAW73314

ID AAW73314 standard; Protein; 515 AA.

XX

AC AAW73314;

XX

DT 08-FEB-1999 (first entry)

XX Parathyroid hormone receptor OK-H.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5840853-A.
 XX
 PD 24-NOV-1998.
 XX
 XX 06-JUN-1995; 95US-0471494.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX
 DR WPI; 1999-034124/03.
 DR N-PSDB; AAV08388.
 XX
 PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX
 PS Claim 6; Fig 1; 63pp; English.
 XX
 CC This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-H, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 515 AA;
 Query Match 4.6%; Score 25; DB 20; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191
 DB 207 GYFRLHCTRNTHMHLFVSFMLRA 231
 RESULT 12
 AAR27705
 ID AAR27705 standard; Protein; 585 AA.
 XX
 AC AAR27705;
 XX
 XX 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
 XX
 KW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia.
 XX
 OS Didelphis virginiana.
 XX
 PN WO9217602-A1.
 XX
 PD 15-OCT-1992.
 XX
 XX 06-APR-1992; 92WO-US02821.
 PF
 XX 05-APR-1991; 91US-0681702.
 PR
 XX 06-APR-1992; 92US-0864475.
 PR

XX (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX
 PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;
 XX
 DR WPI; 1992-366271/44.
 DR N-PSDB; AAQ29605.
 XX
 PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours
 XX
 PS Disclosure; Fig 2; 91pp; English.
 XX
 CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor protein sequence was deduced from the DNA sequence of the
 CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
 CC is identical to the OK-H clone except at the C-terminal tail as OK-O
 CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
 CC The difference is attributed to a single nucleotide deleted in the OK-H
 CC sequence causing a frame shift and an earlier stop codon. It is not
 CC known whether OK-O and OK-H represent prods. of two separate genes or
 CC are a laboratory artifact. The protein may be used in a therapeutic
 CC compen. to inhibit activation of PTH or PTHrP and thus reduce the
 CC level of calcium in the blood. Cpd. capable of competing with PTH
 CC or PTHrP for binding can be identified using the protein prod. and
 CC DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prod. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of
 CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 13; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNTHMHLFVSFMLRA 191
 DB 207 GYFRLHCTRNTHMHLFVSFMLRA 231
 RESULT 13
 AAR92276
 ID AAR92276 standard; Protein; 585 AA.
 XX
 AC AAR92276;
 XX
 XX 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor.
 XX
 KW Parathyroid hormone; receptor; parathormone; PTH;
 KW Parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5494806-A.
 XX
 PD 27-FEB-1996.
 XX
 XX 06-APR-1992; 92US-0864475.
 PF
 XX 06-APR-1992; 92US-0864475.
 PR
 XX 05-APR-1991; 91US-0681702.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX

PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1996-139028/14.
 DR N-PSDB; AAT15946.
 XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.
 XX Claim 1; Fig 2A-2E; 64pp; English.
 PS Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 585 AA;
 SQ Query Match 4.6%; Score 25; DB 17; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLLCTRYIHMLFVSFMLRA 191
 |||||
 Db 207 GYFRRLLCTRYIHMLFVSFMLRA 231
 |||||
 RESULT 14
 AAW73315
 ID AAW73315 standard; Protein; 585 AA.
 AC AAW73315;
 XX 08-FEB-1999 (first entry)
 DT Parathyroid hormone receptor OK-O.
 DE Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 XX PTH-related hypercalcaemia; opossum.
 KW Didelphis virginiana.
 OS US5840853-A.
 XX 24-NOV-1998.
 PD 06-JUN-1995; 95US-0471494.
 PF 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX (GENO) GEN HOSPITAL CORP.
 PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 DR N-PSDB; AAV08389.
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 PT Claim 6; Fig 2; 63pp; English.

XX This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-O, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 20; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLLCTRYIHMLFVSFMLRA 191
 |||||
 Db 207 GYFRRLLCTRYIHMLFVSFMLRA 231
 |||||

RESULT 15
 ABG27219
 ID ABG27219 standard; Protein; 864 AA.
 XX AC ABG27219;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #27210.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS91406.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 57578; 103pp; English.

The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 864 AA;

Query Match 4.1%; Score 22; DB 22; Length 864;
 Best Local Similarity 100.0%; Pred. No. 3.2e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LGASLHVGMWMLGSCCLLARAQ 25
 DB 4 LGASLHVGMWMLGSCCLLARAQ 25
 |||||

RESULT 16
 ABP82552
 ID ABP82552 standard; Peptide; 20 AA.
 XX AC ABP82552;
 XX DT 04-MAR-2003 (first entry)
 XX DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1225.
 XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

OS Homo sapiens.
 XX W0200261087-A2.
 XX PD 08-AUG-2002.
 XX PF 19-DEC-2001; 2001WO-US50107.
 XX PR 19-DEC-2000; 2000US-257144P.
 XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX PI Burmer GC, Roush CL, Brown JP;
 XX DR WPI; 2003-046718/04.
 XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX Claim 1; Fig 2; 523pp; English.

PS The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 20 AA;

Query Match 3.7%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 ESLIMQDDPONSIEATSVDK 230
 DB 1 ESLIMQDDPONSIEATSVDK 20
 |||||

RESULT 17
 AAB08188
 ID AAB08188 standard; Protein; 440 AA.
 XX AC AAB08188;
 XX DT 04-DEC-2000 (first entry)
 XX DE Amino acid sequence of rat secretin receptor polypeptide.
 XX KW Secretin; gastrointestinal hormone; pancreatic fluid; S cell;
 KW pancreatic cell growth; pancreatic beta cell; pancreatic islet;
 KW insulin production; glucose metabolism; insulin resistance;
 KW glucose intolerance; hyperglycemia; hyperinsulinemia; obesity;
 KW hyperlipidemia; hyperproteinemia; Type II diabetes mellitus;
 KW secretin receptor.
 XX OS Rattus sp.
 XX PN W0200047721-A2.
 XX PD 17-AUG-2000.
 XX PF 10-FEB-2000; 2000WO-US03422.
 XX PR 10-FEB-1999; 99US-0119575.
 XX PA (ONTO-) ONTOGENY INC.
 XX PI Kagan D, Pang K;
 XX DR WPI; 2000-515058/46.
 XX DR N-PSDB; AAA63813.
 XX PT Secretin therapeutic is used to modulate the growth state of pancreatic
 PT cells to provide treatment for diabetes through modification of glucose
 PT metabolism -
 XX Disclosure; Page 88-90; 90pp; English.
 XX PS The present sequence represents a rat secretin receptor polypeptide.
 CC Secretin is a gastrointestinal hormone that stimulates the secretion of
 CC bicarbonate-rich pancreatic fluid. Secretin is produced by specific
 CC endocrine cells (S cells) located in the mucosa of the proximal small
 CC intestine. Secretion of secretin is stimulated by the presence of either
 CC acidic pH or fatty acids in the duodenum. The specification describes
 CC a method for modulating the growth state of pancreatic cells. The method

CC comprises contacting the cells with a secretin therapeutic or prodrug
 CC form of secretin. Secretin is used to modulate the growth state of
 CC pancreatic cells, in particular to promote the proliferation of
 CC pancreatic cells, generate functional pancreatic beta cells from
 CC pancreatic islets or cells, promote insulin production in a pancreatic
 CC islet or cell, antagonize insulin inhibition of secretin response in
 CC secretin-responsive cells, modify glucose metabolism in an animal to
 CC treat a disease associated with altered glucose metabolism e.g. insulin
 CC resistance, glucose intolerance or non-responsiveness, hyperglycemia,
 CC hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II
 CC diabetes mellitus (NIDDM).
 XX
 SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 21; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSF 187
 |||||
 Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 18
 ABB56387
 ID ABB56387 standard; Protein; 440 AA.
 XX

AC ABB56387;

DT 18-FEB-2002 (first entry)

DE Non-endogenous human GPCR protein, SEQ ID NO: 567.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX

OS Homo sapiens.

OS Synthetic.

PN WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US11098.

XX 07-APR-2000; 2000US-195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

DR N-PSDB; ABI98023.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -

XX Claim 1; Page 370-371; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.

XX Sequence 440 AA;

Query Match 3.5%; Score 19; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 FRLHCTRNVIHMLFVSF 187
 |||||
 Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 19

AAAB71877
 ID AAB71877 standard; Protein; 440 AA.

AC AAB71877;

DT 03-MAY-2001 (first entry)

DE Human SCRC seven transmembrane domain.

XX Human; SCRC; secretin receptor; h15571; immunomodulatory; vascular;
 KW hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive;
 KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.

OS Homo sapiens.

PN WO200109328-A1.

XX 08-FEB-2001.

XX 03-AUG-2000; 2000WO-US21278.

XX 03-AUG-1999; 99US-0146916.

PR 29-FEB-2000; 2000US-0515781.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hodge MR, Lloyd C, Weich NS;

XX WPI; 2001-138653/14.

XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX Disclosure; Fig 2; 145pp; English.

XX The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases includes immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.

XX Sequence 440 AA;

Query Match 3.5%; Score 19; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSF 187
 |||||

Db 167 FRLHCTRNVIHMLFVSF 185

RESULT 20
 ABE08012
 ID ABB08012 standard; Protein; 440 AA.
 AC ABB08012;
 DT 27-AUG-2002 (first entry)
 DE Protein identified by trembl Accession No. AB109120.
 KW Secretin receptor-like GPCR; G-protein coupled receptor; GPCR; human;
 KW uropathic; cytotonic; antischizophrenic; tranquilliser; antidepressant;
 KW hypotensive; antimigraine; anorectic; nootropic; neuroprotective;
 KW antileptic.
 OS Homo sapiens.
 PN WO200229050-A2.
 PD 11-APR-2002.
 PF 04-OCT-2001; 2001WO-EP11442.
 PR 06-OCT-2000; 2000US-238045P.
 XX 31-AUG-2001; 2001US-315958P.
 PA (FARB) BAYER AG.
 PI Liou J;
 PI WPI; 2002-362601/39.
 DR An isolated polynucleotide encoding a secretin receptor-like G-protein
 XX coupled receptor polypeptide, for identifying reagents which modulate
 PT its function used to treat e.g. obesity, cancer and diabetes -
 PT Disclosure; Fig 3; 133pp; English.
 CC The invention relates to a human secretin receptor-like G-protein coupled
 CC receptor (GPCR) polypeptide and encoding polynucleotide. An expression
 CC vector comprising the polynucleotide is useful for preparing a medicament
 CC for modulating the activity of a secretin receptor-like GPCR in a disease
 CC such as urinary incontinence, benign prostate hyperplasia, obesity,
 CC cancer, diabetes, osteoporosis, anxiety, depression, hypertension,
 CC migraine, compulsive disorder, schizophrenia, autism, a neurodegenerative
 CC disorder, or cancer chemotherapy-induced vomiting. These diseases may
 CC also be treated by reagents which modulate a function of a human secretin
 CC receptor like GPCR, where symptoms of the secretin receptor-like GPCR
 CC dysfunction are ameliorated. The present sequence represents a protein
 CC identified by trembl Accession No. AB109120.
 SQ Sequence 440 AA;
 Query Match 3.5%; Score 19; DB 23; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 169 FRLHCTRNTHMHLFVSF 187
 Db 167 FRLHCTRNTHMHLFVSF 185
 RESULT 21
 ABB1202
 ID ABB1202 standard; Protein; 440 AA.
 AC ABB1202;
 DT 13-AUG-2002 (first entry)
 DE Human secretin receptor-like GPCR related protein SEQ ID NO:3.
 KW Human secretin receptor-like GPCR related protein SEQ ID NO:3.

KW Human; secretin; secretin receptor-like G protein-coupled receptor;
 KW secretin receptor-like GPCR; receptor; uropathic; cytotonic; anorectic;
 KW antidiabetic; osteopathic; tranquilliser; antidepressant; hypotensive;
 KW antimigraine; neuroleptic; nootropic; antileptic; vaccine;
 KW antisense therapy; protein therapy; urinary incontinence; obesity;
 KW benign prostate hyperplasia; cancer; diabetes; osteoporosis; anxiety;
 KW depression; hypertension; migraine; compulsive disorder; schizophrenia;
 KW autism; neurodegenerative disorder.
 XX Homo sapiens.
 OS OS
 PN WO200229051-A2.
 XX 11-APR-2002.
 PD 04-OCT-2001; 2001WO-EP11443.
 PF 06-OCT-2000; 2000US-238043P.
 XX (FARB) BAYER AG.
 PA Liou J;
 PI WPI; 2002-362602/39.
 DR Polynucleotides encoding secretin receptor-like G-Protein Coupled
 XX Receptors, useful for preventing, diagnosing and treating urinary
 PT incontinence, benign prostate hyperplasia, Obesity, or hypertension -
 PT Disclosure; Fig 3; 113pp; English.
 CC The present invention describes a human secretin receptor-like G protein-
 CC coupled receptor (GPCR) (I). (I) has uropathic, cytotonic, anorectic,
 CC antidiabetic, osteopathic, tranquilliser, antidepressant, hypotensive,
 CC antimigraine, neuroleptic, nootropic and antileptic activities. (I) and
 CC the polynucleotide encoding it (II) can be used in gene therapy,
 CC antisense therapy, protein therapy and vaccine production. (I) and (II)
 CC can be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate secretin receptor-like GPCR expression.
 CC Disorders that may be prevented, diagnosed and/or treated by (I) and
 CC (II) include, for example urinary incontinence, benign prostate
 CC hyperplasia, obesity, or a disease related to obesity, cancer,
 CC diabetes, osteoporosis, anxiety, depression, hypertension, migraine,
 CC compulsive disorder, schizophrenia, autism, a neurodegenerative
 CC disorder or cancer chemotherapy-induced vomiting. Human secretin
 CC receptor-like GPCR is located to chromosome 6. The present sequence
 CC represents a protein given in the exemplification of the present
 CC invention.
 XX SQ Sequence 440 AA;
 Query Match 3.5%; Score 19; DB 23; Length 440;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 169 FRLHCTRNTHMHLFVSF 187
 Db 167 FRLHCTRNTHMHLFVSF 185
 RESULT 22
 ABB1912
 ID ABB1912 standard; Protein; 440 AA.
 AC ABB1912;
 DT 04-MAR-2003 (first entry)
 DE Human secretin receptor protein SEQ ID NO:310.
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.

XX Homo sapiens.

OS WO200261087-A2.

XX 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

PI WPI; 2003-046718/04.

DR N-PSDB; AB242760.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases -

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 440 AA;

Query Match

Best Local Similarity 3.5%; Score 19; DB 24; Length 440;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYNHMHLFVSF 187

Db 167 FRRLHCTRYNHMHLFVSF 185

RESULT 23

AAR30187

ID AAR30187 standard; Protein; 449 AA.

XX AAR30187;
 AC 25-MAR-2003 (updated)
 DT 28-APR-1993 (first entry)
 DE Secretin receptor.
 XX Rat; rat/mouse hybridoma; NG 108-15.
 KW Rattus rattus.
 OS
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..22
 FT /note= "signal peptide"
 FT Protein 23..449
 FT /note= "mature secretin receptor"
 FT Modified-site 72
 FT /note= "potential N-glycosylation site"
 FT Modified-site 100
 FT /note= "potential N-glycosylation site"
 FT Modified-site 106
 FT /note= "potential N-glycosylation site"
 FT Modified-site 128
 FT /note= "potential N-glycosylation site"
 FT Modified-site 291
 FT /note= "potential N-glycosylation site"
 FT Domain 144..165
 FT /note= "transmembrane domain"
 FT Domain 175..194
 FT /note= "transmembrane domain"
 FT Domain 217..240
 FT /note= "transmembrane domain"
 FT Domain 254..276
 FT /note= "transmembrane domain"
 FT Domain 294..317
 FT /note= "transmembrane domain"
 FT Domain 343..362
 FT /note= "transmembrane domain"
 FT Domain 374..394
 FT /note= "transmembrane domain"

WO9221754-A1.

10-DEC-1992.

05-JUN-1992; 92WO-JP00728.

07-JUN-1991; 91JP-0163946.

(OSAB-) OSAKA BIOSCIENCE INST.

Ishihara T, Nagata S, Takahashi K;

WPI; 1992-433652/52.

DR N-PSDB; AAQ33018.

PT DNA coding for secretin receptor - is expressed in COS cells and
 PT produces a receptor protein for research and clinical use

PS Claim 2; Fig 1; 44pp; Japanese.

XX The secretin receptor was encoded by a DNA sequence of rat origin,
 CC contained in rat/mouse hybridoma NG108-15. The DNA sequence was
 CC obtd. from a cDNA library derived from NG108-15 cells. Expression
 CC in a suitable host allows prodn. of the receptor protein. The
 CC secretin receptor protein encoded by this gene may be used in basic
 CC research and in clinical tests, and is available in high yield.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 449 AA;

Query Match

3.5%; Score 19; DB 13; Length 449;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTERNYHMLFVSP 187
|||||
Db 167 FRLHCTERNYHMLFVSP 185

RESULT 24

ABP82551
ID ABP82551 standard; Peptide; 18 AA.

AC ABP82551;

DT 04-MAR-2003 (first entry)

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1224.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

OS Homo sapiens.

PN WO200261087-A2.

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US50107.

PR 19-DEC-2000; 2000US-257144P.

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burmer GC, Roush CL, Brown JP;

WPI; 2003-046718/04.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -

PS Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81575 to ABP82018, which are used in the
CC exemplification of the present invention.

SQ Sequence 18 AA;

Query Match 3.3%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 KAKVQCELNITAIQEGE 60
|||||
Db 1 KAKVQCELNITAIQEGE 18

RESULT 25

AA96985
ID AA96985 standard; Protein; 324 AA.

AC AA96985;

DT 19-DEC-2000 (first entry)

DE Tethered PTH-1 receptor, r-del-Nt/Ct.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct;
KW tethered receptor; osteoporosis.

OS Chimeric - Rattus sp.

OS Synthetic.

PN WO200039278-A2.

PD 06-JUL-2000.

PF 30-DEC-1999; 99WO-US31108.

PR 31-DEC-1998; 98US-0114577.

PA (GARD/) GARDELLA T J.

PA (KRON/) KRONENBERG H M.

PA (POTT/) POTTS J T.

PA (JUEP/) JUEPPNER H.

PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

WPI; 2000-452384/39.

DR N-PSDB; AAA51734.

XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass

PS Claim 22; Fig 10; 119pp; English.

XX Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or
CC S-(L)_n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R₁ is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tethered activity,
CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrP which
CC avoids the need for regular injections to treat osteoporosis.

XX

SQ Sequence 324 AA;

Query Match 3.3%; Score 18; DB 21; Length 324;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 134 YFLATNYWILVEGLYLH 151
 |||||

RESULT 26
 AAY96984
 ID AAY96984 standard; Protein; 335 AA.
 XX
 AC AAY96984;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Tethered PTH-1 receptor, Tether1C.
 XX
 KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether1C; osteoporosis.
 XX
 OS Chimeric - Rattus sp.
 XX
 OS Synthetic.
 XX

Key	Location/Qualifiers
Peptide	1..23
Peptide	/label= PTH-1_receptor_signal_sequence
Peptide	24..32
Peptide	/label= PTH_residues_1-9
Peptide	33..36
Peptide	/label= linker
Protein	37..335
Protein	/label= PTH-1_receptor
Protein	/note= "residue 182 to 480"

WO200039278-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 30-DEC-1999; 99WO-US31108.
 XX
 PR 31-DEC-1998; 98US-0114577.
 XX
 PR (GARD/) GARDELLA T J.
 PA (KRON/) KRONENBERG H M.
 PA (PORT/) POTTS J T.
 PA (JUEP/) JUEPPNER H.
 XX
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51733.
 XX
 PT New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 XX
 PS Claim 22; Fig 9; 119pp; English.
 XX
 CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or
 CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrp which
 CC avoids the need for regular injections to treat osteoporosis.

CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrp which
 CC avoids the need for regular injections to treat osteoporosis.
 XX
 SQ Sequence 335 AA;

Query Match 3.3%; Score 18; DB 21; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 145 YFLATNYWILVEGLYLH 162
 |||||

RESULT 27
 AAY96987
 ID AAY96987 standard; Protein; 435 AA.
 XX
 AC AAY96987;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human tethered PTH-1 receptor, hdelNT.
 XX
 KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
 XX
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX
 PN WO200039278-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 30-DEC-1999; 99WO-US31108.
 XX
 PR 31-DEC-1998; 98US-0114577.
 XX
 PR (GARD/) GARDELLA T J.
 PA (KRON/) KRONENBERG H M.
 PA (PORT/) POTTS J T.
 PA (JUEP/) JUEPPNER H.
 XX
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51736.
 XX
 PT New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 XX
 PS Example 4; Fig 18; 119pp; English.
 XX
 CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or
 CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrp which
 CC avoids the need for regular injections to treat osteoporosis.

SQ Sequence 435 AA;
 Query Match 3.3%; Score 18; DB 21; Length 435;

Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
DB 132 YFLATNYWILVEGLYLH 149

RESULT 28

AAB07529
ID AAB07529 standard; Protein; 435 AA.

AC AAB07529;
XX 20-OCT-2000 (first entry)
DE A mutant parathyroid hormone (PTH) receptor designated rdelatnt.
XX
XX Mutant; parathyroid hormone; PTH; receptor; rdelatnt;
KW ligand binding domain.
XX Homo sapiens.
OS

Key Location/Qualifiers
FH Peptide 1..22
FT /note= "signal peptide"
FT 23..435
FT Protein /note= "mature protein"
XX

PN WO200040698-A1.

XX 13-JUL-2000.

XX 31-DEC-1998; 98WO-US27862.

XX 31-DEC-1998; 98WO-US27862.

XX (GEO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX N-PSDB; AAA58932.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a
PT deletion of the extracellular amino-terminus ligand binding domain, of
PT useful in screening assays for identifying agonists and antagonists of
PTH receptor activity -

XX Claim 17; Fig 1; 81pp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH)
CC receptor, designated rdelatnt. The polypeptide is characterised
CC by a deletion of the extracellular amino-terminus ligand binding
CC domain. The receptor has a minimal domain for ligand binding and
CC is, therefore, useful in screening assays designed for the
CC identification of agonists and antagonists of PTH receptor
CC activity.

XX Sequence 435 AA;

Query Match 3.3%; Score 18; DB 21; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
DB 134 YFLATNYWILVEGLYLH 151

RESULT 29

AAY96983
ID AAY96983 standard; Protein; 446 AA.

XX AAY96983;
AC 31-OCT-2000 (first entry)
XX
DT Tethered PTH-1 receptor, Tether1.
DE
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
OS Chimeric - Rattus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32
FT /label= PTH_residues_1-9
FT Peptide 33..36
FT /label= linker
FT Protein 37..446
FT /label= PTH-1_receptor
FT /note= "residue 182 to end"

XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US31108.

XX 31-DEC-1998; 98US-0114577.

XX (CARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

XX N-PSDB; AAA51732.

XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass
PT Claim 22; Fig 7; 119pp; English.

XX Compounds of the structure or formula S-(L) n-B, R_1-S-(L) n-R or
CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tether1 activity,
CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrp which
CC avoids the need for regular injections to treat osteoporosis.

XX Sequence 446 AA;

Query Match 3.3%; Score 18; DB 21; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
DB 145 YFLATNYWILVEGLYLH 162

RESULT 30
 ID AAY96986
 XX AAY96986 standard; Protein; 448 AA.
 AC AAY96986;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human tethered PTH-1 receptor, Tether1.
 XX
 KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
 XX
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT 24..32
 FT /label= PTH(1-9)
 FT 33..36
 FT /label= Linker
 FT 37..448
 FT /label= PTH-1 receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX
 PN WO200039278-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 30-DEC-1999; 99WO-US31108.
 XX
 PR 31-DEC-1998; 98US-0114577.
 XX
 PA (GARD/) GARDELLA T J.
 PA (KRON/) KRONENBERG H M.
 PA (POTT/) POTTS J T.
 PA (JUEP/) JUEPPNER H.
 XX
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51735.
 XX
 PT New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 XX
 PS Example 4; Fig 17; 119pp; English.
 XX
 CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or
 CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC diseases and disorders associated with decreased tether1 activity,
 CC increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrP which
 CC avoids the need for regular injections to treat osteoporosis.
 XX
 SQ Sequence 448 AA;
 Query Match 3.3%; Score 18; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 DB 145 YFLATNYWILVEGLYLH 162
 RESULT 31
 ID AAY96988
 XX AAY96988 standard; Protein; 450 AA.
 AC AAY96988;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human tethered PTH-1 receptor, Tether-R11.
 XX
 KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
 XX
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT 24..34
 FT /label= PTH(1-11)
 FT 35..38
 FT /label= Linker
 FT 39..450
 FT /label= PTH-1 receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX
 PN WO200039278-A2.
 XX
 PD 06-JUL-2000.
 XX
 PF 30-DEC-1999; 99WO-US31108.
 XX
 PR 31-DEC-1998; 98US-0114577.
 XX
 PA (GARD/) GARDELLA T J.
 PA (KRON/) KRONENBERG H M.
 PA (POTT/) POTTS J T.
 PA (JUEP/) JUEPPNER H.
 XX
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX
 DR WPI; 2000-452384/39.
 DR N-PSDB; AAA51737.
 XX
 PT New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass
 XX
 PS Example 4; Fig 19; 119pp; English.
 XX
 CC Compounds of the structure or formula S-(L) n-B, R1-S-(L) n-R or
 CC S-(L) n-R, are new. S is an amino terminal signaling functional domain
 CC of parathyroid hormone (PTH); L is a linker molecule present n times
 CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
 CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
 CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
 CC receptor sequence. The new compounds are used for treating mammalian
 CC conditions characterized by decreases in bone mass, determining rates of
 CC bone reformation, bone resorption and/or bone remodeling, treating
 CC diseases and disorders associated with decreased tether1 activity,
 CC increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
 CC for a peptide or non-peptide PTH (claimed). The new compound can be
 CC administered by inhalation unlike the large native PTH or PTHrP which
 CC avoids the need for regular injections to treat osteoporosis.
 XX

SQ Sequence 450 AA;
 Query Match 3.3%; Score 18; DB 21; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
 Db 147 YFLATNYWILVEGLYH 164
 |||||
 |||||

RESULT 32
 AAY99600
 ID AAY99600 standard; Protein; 536 AA.
 XX
 AC AAY99600;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE Zebrafish parathyroid hormone type-1 receptor PTH1R.
 XX
 KW Zebrafish; parathyroid hormone type-1 receptor; PTH1R;
 KW developmental disorder; physiological disorder; neurological disorder.
 XX
 OS Brachydanio rerio.
 XX
 PN WO200032775-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US28207.
 XX
 PR 30-NOV-1998; 98US-0110467.
 XX
 PA (JUEP/) JUEPPNER H.
 PA (RUBI/) RUBIN D A.
 XX
 PI Jueppner H, Rubin DA;
 XX
 DR WPI; 2000-412323/35.
 DR N-PSDB; AAA49625.
 XX
 PT New nucleic acids encoding parathyroid hormone receptors PTH1R and
 PT PTH3R, useful for treating diseases or disorders associated with
 PT impaired receptor functions comprises a specific nucleotide sequence -
 XX
 PS Claim 17; Fig 2A; 111pp; English.
 XX
 CC The present sequence is the parathyroid hormone type-1 receptor
 CC (PTH1R) from the zebrafish. Its coding sequence was obtained by
 CC sequencing a cDNA clone. The gene and protein can be used to detect
 CC diseases in man where the receptor is either overexpressed or
 CC underexpressed, and they can be used to treat these diseases, which may
 CC be developmental, physiological or neurological disorders. They can also
 CC be used to identify agonists and antagonists which can be used in a
 CC similar manner. In addition, the gene can be used for chromosome
 CC identification.
 XX
 SQ Sequence 536 AA;
 Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 2.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNHMLF 184
 Db 167 GYFRLHCTRYNHMLF 184
 |||||
 |||||

RESULT 33
 AAY90230
 ID AAY90230 standard; Protein; 536 AA.
 XX

AC AAY90230;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Zebrafish PTH1R receptor protein sequence.
 XX
 KW Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;
 KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
 XX
 OS Brachydanio rerio.
 XX
 PN WO200032771-A1.
 XX
 PD 08-JUN-2000.
 XX
 PF 28-MAY-1999; 99WO-US11883.
 XX
 PR 30-NOV-1998; 98US-0110467.
 XX
 PA (JUEP/) JUEPPNER H.
 PA (RUBI/) RUBIN D A.
 XX
 PI Jueppner H, Rubin DA;
 XX
 DR WPI; 2000-412319/35.
 DR N-PSDB; AAA30828.
 XX
 PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
 PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
 PT hormone receptor 1 for treating disorders associated with receptor
 PT function -
 XX
 PS Claim 17; Fig 2a; 111pp; English.
 XX
 CC This sequence is a parathyroid hormone receptor type 1 (PTH1R)
 CC receptor protein of the invention. The invention also relates to a PTH3R
 CC receptor protein. Antagonists of PTH1R or PTH3R can be used for the
 CC treatment of diseases associated with an increase in PTH1R or PTH3R
 CC activity, respectively. The peptides are used for diagnosis or prognosis
 CC of diseases and disorders associated with PTH3R or PTH1R, such as cancer.
 CC The polypeptides can be used as a molecular weight markers on sodium
 CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
 CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
 CC peptides and polypeptides are useful to raise antibodies, including
 CC monoclonal antibodies, that bind specifically to a polypeptide. The
 CC peptides are useful during diagnosis of diseases and disorders in
 CC mammals involving PTH1R or PTH3R receptor expression or function.
 CC Mutations that affect PTH1R or PTH3R sequence and/or expression levels
 CC of PTH1R or PTH3R could be diagnostic for patients with disease or
 CC disorders of a developmental, physiological or neurological nature. The
 CC nucleic acid molecules are valuable for chromosome identification. The
 CC mapping of DNAs to chromosomes is an important first step in
 CC correlating those sequences with genes associated with disease.
 XX
 SQ Sequence 536 AA;
 Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 2.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNHMLF 184
 Db 167 GYFRLHCTRYNHMLF 184
 |||||
 |||||

RESULT 34
 AAR27706
 ID AAR27706 standard; Protein; 591 AA.
 XX
 AC AAR27706;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)


```

Query Match      3.3%; Score 18; DB 17; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
    |||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 36
AAW73316
ID AAW73316 standard; Protein; 591 AA.
AC AAW73316;
XX
DT 08-FEB-1999 (first entry)
XX
DE Parathyroid hormone receptor R15B.
XX
KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; rat.
XX
OS Rattus sp.
XX
PN US5840853-A.
XX
PD 24-NOV-1998.
XX
PF 06-JUN-1995; 95US-0471494.
XX
PR 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
PR 06-JUN-1995; 95US-0471494.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
DR WPI; 1999-034124/03.
DR N-PSDB; AAV08390.
XX
PT Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX
PS Claim 6; Fig 3; 63pp; English.
XX
CC This sequence represents the rat parathyroid hormone (PTH) receptor
CC R15B, which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX
SQ Sequence 591 AA;

Query Match      3.3%; Score 18; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
    |||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 37
AAR22278
ID AAR22278 standard; Protein; 593 AA.
XX
AC AAR22278;
XX
DT 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)

```

```

XX DE Human kidney PTH/PTHrP receptor.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer.
XX OS Homo sapiens.
XX PN US5494806-A.
XX PD 27-FEB-1996.
XX PF 06-APR-1992; 92US-0864475.
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX DR WPI; 1996-139028/14.
XX DR N-PSDB; AAT15948.
XX
PT DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
XX
PS Claim 1; Fig 6A-6G; 64pp; English.
XX
CC A human parathyroid hormone/parathyroid hormone-related protein
CC (PTH/PTHrP) receptor (AAR92278) is encoded by cDNA clone HK-1
CC (AAT15948) isolated from a human kidney cDNA library. The receptor
CC induces an increase in intracellular cAMP and intracellular free
CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
CC be produced in vector/host cell systems and used in the treatment,
CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
CC screen for (ant)agonists and to raise antibodies. Host cells
CC expressing the receptor can be used for diagnostic measurement of
CC PTH serum levels.
XX
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 593 AA;

Query Match      3.3%; Score 18; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
    |||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 38
AAW73317
ID AAW73317 standard; Protein; 593 AA.
XX
AC AAW73317;
XX
DT 08-FEB-1999 (first entry)
XX
DE Human Parathyroid hormone receptor.
XX
KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; human.
XX
OS Homo sapiens.
XX
PN US5840853-A.
XX
PD 24-NOV-1998.

```

XX PF 06-JUN-1995; 95US-0471494.
 XX PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 XX PR 06-JUN-1995; 95US-0471494.
 PA (GEO) GEN HOSPITAL CORP.
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 DR N-PSDB; AAV08391.
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX Claim 7; Fig 6; 63pp; English.
 XX This sequence represents the human parathyroid hormone (PTH) receptor
 CC which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX Sequence 593 AA;
 SQ Query Match 3.3%; Score 18; DB 20; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWILVEGLYLH 262
 DB 290 YFLATNYWILVEGLYLH 307
 |||||
 RESULT 39
 ABB56385
 ID ABB56385 standard; Protein; 593 AA.
 AC ABB56385;
 XX 18-FEB-2002 (first entry)
 XX Non-endogenous human GPCR protein, SEQ ID NO: 563.
 DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200177172-A2.
 PN 18-OCT-2001.
 PD 05-APR-2001; 2001WO-US11098.
 XX 07-APR-2000; 2000US-195747P.
 XX (AREN-) ARENA PHARM INC.
 PA Lehmann-Bruinsma K, Liaw CW, Lin I;
 PI WPI; 2001-648759/74.
 XX N-PSDB; ABI98021.
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 PT versions of GPCRs -

PS Claim 1; Page 364-366; 394pp; English.
 XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.
 XX Sequence 593 AA;
 SQ Query Match 3.3%; Score 18; DB 22; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWILVEGLYLH 262
 DB 290 YFLATNYWILVEGLYLH 307
 |||||
 RESULT 40
 AAB71876
 ID AAB71876 standard; Protein; 593 AA.
 XX AAB71876;
 AC 03-MAY-2001 (first entry)
 XX Human PTHR seven transmembrane domain.
 DE Human; parathyroid hormone/parathyroid hormone-related peptide receptor;
 KW PTHR; h15571; immunomodulatory; vascular; hepatic; antiasthma;
 KW antimicrobial; antiinflammatory; immunosuppressive; Gene therapy;
 KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
 XX Homo sapiens.
 OS WO200109328-A1.
 PN 08-FEB-2001.
 XX 03-AUG-2000; 2000WO-US21278.
 PF 03-AUG-1999; 99US-0146916.
 PR 29-FEB-2000; 2000US-0515781.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Hodge MR, Lloyd C, Weich NS;
 PI WPI; 2001-138653/14.
 DR Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
 PT -
 XX Disclosure; Fig 2; 145pp; English.
 XX The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases include immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify

CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.

XX Sequence 593 AA;

Query Match 3.3%; Score 18; DB 22; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YPLATNYWILVEGLYLH 262
 |||||
 Db 290 YPLATNYWILVEGLYLH 307

RESULT 41

ABP81872
 ID ABP81872 standard; Protein; 593 AA.

XX AC ABP81872;

XX DT 04-MAR-2003 (first entry)

XX DE Human parathyroid hormone receptor 1 protein SEQ ID NO:229.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42719.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 593 AA;

Query Match 3.3%; Score 18; DB 24; Length 593;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YPLATNYWILVEGLYLH 262
 |||||
 Db 290 YPLATNYWILVEGLYLH 307

RESULT 42

ABG73825
 ID ABG73825 standard; Protein; 595 AA.

XX AC ABG73825;

XX DT 02-APR-2003 (first entry)

XX DE Canine parathyroid hormone 1 receptor, PTHL.

XX dog; parathyroid hormone 1; receptor; PTHL; hypercalcaemia; PTHrP;
 KW hypocalcaemia; PTH mediated hypercalcaemia;
 KW parathyroid hormone related protein; PTHrP mediated hypercalcaemia;
 KW local osteolytic hypercalcaemia; malignancy-related hypercalcaemia;
 KW G-protein coupled receptor family.

XX Canis sp.

XX Key Location/Qualifiers
 XX Region 250..262
 XX /note= "Anti-PTHl antibody epitope region"

XX US2002146777-A1.

XX 10-OCT-2002.

XX 30-AUG-2001; 2001US-0943446.

XX 30-AUG-2000; 2000US-229170P.

XX (CAST/) CASTLEBERRY T A.

XX (LJBB/) LJ B.

XX (OWEN/) OWEN T A.

XX (SMOC/) SMOCK S L.

XX Castleberry TA, Lu B, Owen TA, Smock SL;

XX WPI; 2003-174177/17.

XX N-PSDB; ABX15515.

XX Isolated proteinaceous molecule having canine parathyroid hormone 1
 PT receptor activity used, e.g. for veterinary purposes to treat dogs,
 PT comprises naturally occurring canine peptide -
 XX Claim 1; Fig 1; 17pp; English.

CC The invention relates to an isolated proteinaceous molecule having canine
 CC parathyroid hormone 1 receptor (PTHr) activity, comprising naturally
 CC occurring canine peptide or naturally occurring canine peptide having one
 CC or more conservative substitutions. PTHr is a member of the G-protein
 CC coupled receptor family. The molecules can be used, e.g. for
 CC veterinary purposes to treat dogs. The polypeptides are useful for the
 CC diagnosis, classification, prognosis, and/or treatment of canine
 CC disorders which may be characterised as related to the interaction
 CC between a cell receptor and its specific ligand, e.g. some forms of
 CC hypercalcaemia and hypocalcaemia. The polypeptides are useful for
 CC distinguishing between hypercalcaemic conditions e.g. PTHr mediated
 CC hypercalcaemia, parathyroid hormone related protein (PTHrP) mediated
 CC hypercalcaemia, hypercalcaemia which does not involve these factors
 CC (local osteolytic hypercalcaemia) and malignancy-related hypercalcaemia.
 CC Large quantities of proteinaceous molecules having canine PTHr activity
 CC can be produced. The present sequence represents the amino acid sequence
 CC of canine parathyroid hormone 1 receptor, PTHr.

SQ Sequence 595 AA;
 Query Match 3.3%; Score 18; DB 24; Length 595;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 289 YFLATNYWILVEGLYLH 306

RESULT 43
 AAR27707
 ID AAR27707 standard; Protein; 614 AA.

AC AAR27707;
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)
 DE Human kidney PTH/PTHrP receptor.

XW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia.

OS Homo sapiens.

PN W09217602-A1.

PD 15-OCT-1992.

PF 06-APR-1992; 92WO-US02821.

PR 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;

DR WPI; 1992-366271/44.

DR N-PSDB; AAQ29607.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours

PS Claim 22; Fig 6; 91pp; English.

XX The protein sequence was deduced from the cDNA sequence obtd by
 CC screening a human kidney oligo dT-primed cDNA library in lambda
 CC gt10 and a genomic library of human placental DNA in EMBL3 with a
 CC probe comprising most of the coding sequence of rat bone parathyroid
 CC hormone/parathyroid hormone related protein (PTH/PTHrP) receptor

CC protein. The clone encodes a protein which may be used in a
 CC therapeutic compsn. to inhibit activation of PTH or PTHrP and thus
 CC reduce the level of calcium in the blood. Cps. capable of competing
 CC with PTH or PTHrP for binding can be identified using the protein prod.
 CC and DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of
 CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also R27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 614 AA;

Query Match 3.3%; Score 18; DB 13; Length 614;
 Best Local Similarity 100.0%; Pred. No. 3e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 44
 ABB79169
 ID ABB79169 standard; protein; 447 AA.

AC ABB79169;

DT 07-AUG-2002 (first entry)

DE Carassius auratus VPAC1 receptor protein SEQ ID NO:9.

XW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;
 KW vasoactive intestinal peptide; muscle mass regulation; antibacterial;
 KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;
 KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;
 KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;
 KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.

OS Carassius auratus.

PN W0200235240-A2.

PD 02-MAY-2002.

PF 22-OCT-2001; 2001WO-US43882.

PR 23-OCT-2000; 2000US-0694519.

PA (PROC) PROCTER & GAMBLE CO.

PI Isfort RJ, Sheldon RJ;

DR WPI; 2002-471451/50.

PT Identifying candidate compounds for regulating skeletal muscle mass or
 PT function by contacting test compound with vasoactive intestinal peptide
 PT receptors or cell expressing the receptor -

PS Disclosure; Page 76-77; 87pp; English.

XX The present invention describes a method for identifying candidate
 CC compounds (CC) for regulating skeletal muscle mass or function. The
 CC method involves contacting a test compound (TC) with a vasoactive
 CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor
 CC and determining whether TC binds to VPAC receptor or TC that activates
 CC the VPAC receptors, where the TC that binds to or activates VPAC is
 CC identified as CC. The method can be used for identifying CC for
 CC regulating skeletal mass or function. Other methods from the present
 CC invention can be used for: identifying CC that prolong or augment the
 CC activation of VPAC receptor or VPAC receptor signal transduction pathway;
 CC identifying CC for increasing VPAC receptor expression; identifying CC
 CC for increasing the expression of vasoactive intestinal peptide (VIP) or a

CC VIP analogue; increasing skeletal mass or function in a subject; and for
 CC treating skeletal muscle atrophy in a subject. A pharmaceutical
 CC composition comprising a safe and effective amount of a VPAC receptor
 CC agonist can be used for modulating skeletal muscle atrophy which includes
 CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
 CC broken bones, denervation/nerve damage due to spinal cord injury,
 CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
 CC conditions, sepsis due to infection or other causes, nutrient limitation
 CC due to illness or starvation, cancer, cachexia, chronic inflammation,
 CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
 CC disorders, e.g., muscular dystrophies, neurodegenerative diseases.
 CC The present sequence represents a VPAC1 receptor which is given
 CC in the exemplification of the present invention.

XX SQ Sequence 447 AA;

Query Match 3.0%; Score 16; DB 23; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNHYHMLFVSF 187
 |||||
 Db 131 LHCTRNHYHMLFVSF 146

RESULT 45

AAR27710
 ID AAR27710 standard; peptide; 19 AA.

XX AC AAR27710;

DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)

XX PTH/PTHrP receptor fragment.

KW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia; extracellular domain.

XX Synthetic.

XX WO9217602-A1.

XX 15-OCT-1992.

XX 06-APR-1992; 92WO-US02821.

XX 05-APR-1991; 91US-0681702.

XX 06-APR-1992; 92US-0864475.

XX (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 XX Segre GV;

XX WPI; 1992-366271/44.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
 XX - for (differential) diagnosis of hypercalcaemia, and diagnosis
 XX and treatment of tumours

XX Claim 25; Page 5; 9ipp; English.

XX The peptide sequence shown represents an extracellular fragment of
 CC parathyroid hormone/parathyroid hormone related protein
 CC (PTH/PTHrP) receptor protein. The peptide is capable of binding
 CC PTH or PTHrP and acting as an antagonist of these cpds. The
 CC peptide may be used to inhibit activation of PTH or PTHrP and thus
 CC reduce the level of calcium in the blood. Cpds. capable of competing
 CC with PTH or PTHrP for binding can be identified using the protein prod.
 CC and DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of

CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYYWILVEG 258
 |||||
 Db 6 YFLATNYYWILVEG 19

RESULT 46

AAR92281
 ID AAR92281 standard; Peptide; 19 AA.

XX AC AAR92281;

DT 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)

XX PTH/PTHrP extracellular region fragment RP-3.

KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer.

XX Synthetic.

XX US5494806-A.

XX 27-FEB-1996.

XX 06-APR-1992; 92US-0864475.

XX 06-APR-1992; 92US-0864475.

XX 05-APR-1991; 91US-0681702.

XX (GEHO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 XX Schipani E, Segre GV;

XX WPI; 1996-139028/14.

XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 XX diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 XX cancer etc.

XX Claim 21; Column 3; 64pp; English.

XX Parathyroid hormone (PTH) receptor fragments, including those
 CC (AAR92279-84) based on the PTH extracellular region and those
 CC (AAR92285-87) based on the intracellular domain, are produced by
 CC incorporating encoding DNA sequences into a vector, and
 CC culturing cells transformed by the vector. The peptides can be
 CC used to raise antibodies. The peptides and antibodies are useful
 CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
 CC hypocalcaemia, and can also be used to screen for (ant)agonists
 CC of therapeutic appln.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYYWILVEG 258
 |||||

Db 6 YFLATNYWILVEG 19

RESULT 47
AAW73320
ID AAW73320 standard; peptide; 19 AA.
XX
AC AAW73320;
XX
DT 08-FEB-1999 (first entry)
XX
DE Parathyroid hormone receptor fragment RP-3.
XX
KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; opossum; rat; human.
XX
OS Synthetic.
XX
PN US5840853-A.
XX
PD 24-NOV-1998.
XX
PF 06-JUN-1995; 95US-0471494.
XX
PR 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
PR 06-JUN-1995; 95US-0471494.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
DR WPI; 1999-034124/03.
XX
PT Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX
PS Claim 8; Column 19; 63pp; English.
XX
CC This sequence is a fragment of a opossum parathyroid hormone (PTH)
CC receptor which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX
SQ Sequence 19 AA;
Query Match 2.6%; Score 14; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEG 258
DB 6 YFLATNYWILVEG 19
RESULT 48
ABB79166
ID ABB79166 standard; protein; 444 AA.
XX
AC ABB79166;
XX
DT 07-AUG-2002 (first entry)
XX
DE Rana ridibunda VPAC1 receptor protein SEQ ID NO:6.
XX
KW VPAC receptor; vasoactive intestinal peptide receptor; VIP; cytostatic;
KW vasoactive intestinal peptide; muscle mass regulation; antibacterial;
KW immunosuppressive; immunomodulator; antiinflammatory; infection; sepsis;
KW skeletal muscle atrophy; autoimmune disease; infectious disease; cancer;
KW cachexia; chronic inflammation; congestive heart failure; sarcopenia;

KW AIDS; genetic disorder; muscular dystrophy; neurodegenerative disease.
XX
OS Rana ridibunda.
XX
PN WO200235240-A2.
XX
PD 02-MAY-2002.
XX
PF 22-OCT-2001; 2001WO-US43882.
XX
PR 23-OCT-2000; 2000US-0694519.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Isfort RJ, Sheldon RJ;
XX
XX WPI; 2002-471451/50.
XX
PT Identifying candidate compounds for regulating skeletal muscle mass or
PT function by contacting test compound with vasoactive intestinal peptide
PT receptors or cell expressing the receptor -
XX
PS Disclosure; Page 71-73; 87pp; English.
XX
CC The present invention describes a method for identifying candidate
CC compounds (CC) for regulating skeletal muscle mass or function. The
CC method involves contacting a test compound (TC) with a vasoactive
CC intestinal peptide receptors (VPAC) or cell expressing VPAC receptor
CC and determining whether TC binds to VPAC receptor or TC that activates
CC the VPAC receptors, where the TC that binds to or activates VPAC is
CC identified as CC. The method can be used for identifying CC for
CC regulating skeletal mass or function. Other methods from the present
CC invention can be used for: identifying CC that prolong or augment the
CC activation of VPAC receptor or VPAC receptor signal transduction pathway;
CC identifying CC for increasing VPAC receptor expression; identifying CC
CC for increasing the expression of vasoactive intestinal peptide (VIP) or a
CC VIP analogue; increasing skeletal mass or function in a subject; and for
CC treating skeletal muscle atrophy in a subject. A pharmaceutical
CC composition comprising a safe and effective amount of a VPAC receptor
CC agonist can be used for modulating skeletal muscle atrophy which includes
CC skeletal muscle atrophy induced by disuse due to surgery, bed rest,
CC broken bones, denervation/nerve damage due to spinal cord injury,
CC autoimmune disease, infectious disease, glucocorticoid use for unrelated
CC conditions, sepsis due to infection or other causes, nutrient limitation
CC due to illness or starvation, cancer, cachexia, chronic inflammation,
CC AIDS cachexia, COPD, congestive heart failure, sarcopenia and genetic
CC disorders, e.g., muscular dystrophies, neurodegenerative diseases.
CC The present sequence represents a VPAC1 receptor which is given
CC in the exemplification of the present invention.
XX
SQ Sequence 444 AA;
Query Match 2.4%; Score 13; DB 23; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRYIHMLF 184
DB 157 LHCTRYIHMLF 169
RESULT 49
ABB56393
ID ABB56393 standard; Protein; 457 AA.
XX
AC ABB56393;
XX
DT 18-FEB-2002 (first entry)
XX
DE Non-endogenous human GPCR protein, SEQ ID NO: 579.
XX
KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW constitutively activated GPCR; agonist; disease.

XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200177172-A2.
XX PD 18-OCT-2001.
XX PF 05-APR-2001; 2001WO-US11098.
XX PR 07-APR-2000; 2000US-195747P.
XX PA (AREN-) ARENA PHARM INC.
XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX DR WPI; 2001-648759/74.
XX DR N-PSDB; ABI98029.
XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX PT disease treatment, comprises contacting candidate compounds with
XX PT versions of GPCRs -
XX PS Claim 1; Page 381-383; 394pp; English.
XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
XX CC the endogenous ligand has been identified. Non-endogenous
XX CC constitutively activated versions of known GPCRs are used in the
XX CC invention for the direct identification of candidate compounds as
XX CC receptor agonists, inverse agonists or partial agonists. Such
XX CC agonists are useful as therapeutic agents for diseases or disorders
XX CC associated with GPCRs. The present sequence is a non-endogenous
XX CC version of a known human GPCR.
XX SQ Sequence 457 AA;
Query Match 2.4%; Score 13; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182
RESULT 50
ID AAB71878
ID AAB71878 standard; Protein; 457 AA.
XX AC AAB71878;
XX DT 03-MAY-2001 (first entry)
XX DE Human VIPR seven transmembrane domain.
XX KW Human; h15571; immunomodulatory; vascular; hepatic; antiasthma; VIPR;
XX KW pituitary adenylate cyclase activating polypeptide type II receptor;
XX KW antimicrobial; antiinflammatory; immunosuppressive; gene therapy;
XX KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
XX KW respiratory disorder; infection; chronic inflammatory disease;
XX KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
XX OS Homo sapiens.
XX PN WO200109328-A1.
XX PD 08-FEB-2001.
XX PF 03-AUG-2000; 2000WO-US21278.
XX PR 03-AUG-1999; 99US-0146916.
XX PR 29-FEB-2000; 2000US-0515781.

PA (MILL-) MILLENNIUM PHARM INC.
XX PI Hodge MR, Lloyd C, Weich NS;
XX DR WPI; 2001-138653/14.
XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
XX PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX PS Disclosure; Fig 2; 145pp; English.
XX CC The present sequence is a human G-protein coupled receptor (GPCR) used
XX CC for comparison with the seven transmembrane domain of a novel GPCR
XX CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
XX CC used in the prevention, treatment and diagnosis of diseases associated
XX CC with inappropriate GPCR expression. Such diseases includes immune,
XX CC haematological, fibrotic, hepatic and respiratory disorders including
XX CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
XX CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
XX CC graft rejection, graft versus host disease, cystic fibrosis and, in
XX CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
XX CC in the production of antibodies against GPCR and in assays to identify
XX CC modulators (agonists and antagonists) of GPCR expression and activity.
XX CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
XX CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
XX CC used as diagnostic agents for detecting the presence of GPCR
XX CC polypeptides in samples.
XX SQ Sequence 457 AA;
Query Match 2.4%; Score 13; DB 22; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182
Search completed: December 9, 2003, 09:00:43
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:59:50 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLVWGMLGSL.....DDLMEKPSRPMESNPDTEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS COMB pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	3	US-08-468-011A-2
2	541	100.0	541	4	US-09-236-468A-2
3	541	100.0	541	5	PCT-US95-07085-2
4	60	11.1	60	3	US-08-468-011A-9
5	60	11.1	60	3	US-08-468-011A-11
6	60	11.1	60	3	US-08-468-011A-15
7	60	11.1	60	3	US-08-468-011A-19
8	60	11.1	60	4	US-09-236-468A-9
9	60	11.1	60	4	US-09-236-468A-11
10	60	11.1	60	4	US-09-236-468A-15
11	60	11.1	60	4	US-09-236-468A-19
12	59	10.9	59	3	US-08-468-011A-23
13	59	10.9	59	4	US-09-236-468A-23
14	52	9.6	52	4	US-09-236-468A-13
15	37	6.8	37	3	US-08-468-011A-25
16	37	6.8	37	4	US-09-236-468A-25
17	37	6.8	37	3	US-08-468-011A-13
18	27	5.0	27	5	US-09-449-632-5
19	25	4.6	60	3	US-08-468-011A-20
20	25	4.6	60	4	US-09-236-468A-20
21	25	4.6	515	2	US-08-468-249A-18
22	25	4.6	585	1	US-08-142-439A-6
23	25	4.6	585	2	US-08-142-551B-125
24	25	4.6	585	2	US-08-869-477-6
25	25	4.6	585	2	US-08-468-249A-19
26	21	3.9	21	3	US-08-468-011A-21
27	21	3.9	21	4	US-09-236-468A-21

28 19 3.5 449 1 US-08-142-439A-5 Sequence 5, Appl
29 19 3.5 449 2 US-08-869-477-5 Sequence 5, Appl
30 18 3.3 536 4 US-09-449-632-2 Sequence 2, Appl
31 18 3.3 591 2 US-08-468-249A-20 Sequence 2, Appl
32 18 3.3 593 2 US-08-468-249A-21 Sequence 20, Appl
33 14 2.6 19 1 US-07-864-475A-7 Sequence 21, Appl
34 14 2.6 19 2 US-08-468-249A-7 Sequence 7, Appl
35 14 2.6 60 3 US-08-468-011A-10 Sequence 10, Appl
36 14 2.6 60 4 US-09-236-468A-10 Sequence 10, Appl
37 13 2.4 458 1 US-08-112-817C-2 Sequence 2, Appl
38 13 2.4 1324 2 US-08-811-897A-56 Sequence 56, Appl
39 13 2.4 1324 4 US-09-201-474-56 Sequence 56, Appl
40 12 2.2 445 4 US-09-414-189-1 Sequence 1, Appl
41 11 2.0 542 4 US-09-449-632-4 Sequence 4, Appl
42 10 1.8 10 3 US-08-468-011A-17 Sequence 17, Appl
43 10 1.8 10 4 US-09-236-468A-17 Sequence 17, Appl
44 10 1.8 162 1 US-08-453-956-18 Sequence 18, Appl
45 10 1.8 162 1 US-08-086-631-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSES: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-2

Query Match 100.0%; Score 541; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGAHLVWGMLGSLARQLDSGTTIEQIVLAKVQCELMITAQLQEGE 60
|||||

```
Db 1 MAMLGASLHVWGLMGLSCLLARAQLDSDGTITIEQIVLVKAKVQCELNITQAQOEGE 60
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
Db 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
QY 121 NYSDCLEFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH 180
Db 121 NYSDCLEFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPONS TEATSVDKSOYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPONS TEATSVDKSOYIGCKIAV 240
QY 241 VMIYIYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
Db 241 VMIYIYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHYIVFVCLPHSFSTGLGWEIRMHCELFNFSSFOGFFVSIICYCNGEV 420
Db 361 LAKSTLVLVLVFGVHYIVFVCLPHSFSTGLGWEIRMHCELFNFSSFOGFFVSIICYCNGEV 420
QY 421 QAEVKQWGRWNLISVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRWNLISVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRSNKEDSGRQDDILMEKSRPMESNPDTE 540
Db 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRSNKEDSGRQDDILMEKSRPMESNPDTE 540
QY 541 G 541
Db 541 G 541

RESULT 2
US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match 100.0%; Score 541; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMLGASLHVWGLMGLSCLLARAQLDSDGTITIEQIVLVKAKVQCELNITQAQOEGE 60
Db 1 MAMLGASLHVWGLMGLSCLLARAQLDSDGTITIEQIVLVKAKVQCELNITQAQOEGE 60
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
Db 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
QY 121 NYSDCLEFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH 180
Db 121 NYSDCLEFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH 180
```

```
Db 121 NYSDCLEFLQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPONS TEATSVDKSOYIGCKIAV 240
Db 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMQDDPONS TEATSVDKSOYIGCKIAV 240
QY 241 VMIYIYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
Db 241 VMIYIYFLATNYWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAAFVAAWAVARAT 300
QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLVFGVHYIVFVCLPHSFSTGLGWEIRMHCELFNFSSFOGFFVSIICYCNGEV 420
Db 361 LAKSTLVLVLVFGVHYIVFVCLPHSFSTGLGWEIRMHCELFNFSSFOGFFVSIICYCNGEV 420
QY 421 QAEVKQWGRWNLISVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRWNLISVDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRSNKEDSGRQDDILMEKSRPMESNPDTE 540
Db 481 SPADSLTATSLYLAMSGVTQSRFASHTLSTRSNKEDSGRQDDILMEKSRPMESNPDTE 540
QY 541 G 541
Db 541 G 541

RESULT 3
PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2
```

```
Query Match      100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLASLHVWGLMGLSCILARAQLDSDGTITIEQIVLVKAKVQCELNITQAQLEGE 60
DB 1 MAWLGLASLHVWGLMGLSCILARAQLDSDGTITIEQIVLVKAKVQCELNITQAQLEGE 60
QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
DB 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSDCILRFLOPDISIGKQECERLYVMYTVGVYSISFGLSLAVAILIIGYFRRLHCTRYTH 180
DB 121 NYSDCILRFLOPDISIGKQECERLYVMYTVGVYSISFGLSLAVAILIIGYFRRLHCTRYTH 180
QY 181 MHLFVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSOYIGCKIAV 240
DB 181 MHLFVSMFLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDKSOYIGCKIAV 240
QY 241 VMFIYPLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAAFVAWAVARAT 300
DB 241 VMFIYPLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGPAAAFVAWAVARAT 300
QY 301 LADARCWELSGDIKIYQAPILAAIGLNFILFNTVRVLATKIMETNAVGHDTRKQYRK 360
DB 301 LADARCWELSGDIKIYQAPILAAIGLNFILFNTVRVLATKIMETNAVGHDTRKQYRK 360
QY 361 LAKSTLVVLVGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFFVSIYCYCNGEV 420
DB 361 LAKSTLVVLVGVHYIVFVCLPHSFTGLGWEIRHCELFNSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLVDWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
DB 421 QAEVKKMSRWNLVDWKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYAMSGVTOQTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
DB 481 SPADSLTATSLYAMSGVTOQTASHTLSTRNKEDSGRQDDILMEKPSRPWESNPDT 540
QY 541 G 541
DB 541 G 541

RESULT 4
US-08-468-011A-9
; Sequence 9, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-9

Query Match      100.0%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 IMQDDPONSIEATSVDKSOYIGCKIAVVMFIYPLATNYWILVEGLYHNLIFVAFPSDT 273
DB 1 IMQDDPONSIEATSVDKSOYIGCKIAVVMFIYPLATNYWILVEGLYHNLIFVAFPSDT 60

RESULT 5
US-08-468-011A-11
; Sequence 11, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-11

Query Match      11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy		274 KYLWGFIICWGPFAAFVAAWAVARATLADARCWEISAGDIKWYQAIPILAAIGLNFLF 333
Db		1 KYLWGFIICWGPFAAFVAAWAVARATLADARCWEISAGDIKWYQAIPILAAIGLNFLF 60

RESULT 6

```

US-08-468-011A-15
; Sequence 15, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Roen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-15

```

PRECIPITATION 7

US-08-468-011A-19
; Sequence 19, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
;

PRECIPITATION 7

```

Query Match      11.1%; Score 60; DB 4; Length 60;
Best local Similarity 100%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      214 IMQDDPQNSIEATSDKQYIGCKIAVVMFIYFLATNTYWIILVEGLYHLNLIYFAFFSDT 273
Db      1 IMQDDPQNSIEATSDKQYIGCKIAVVMFIYFLATNTYWIILVEGLYHLNLIYFAFFSDT 60

RESULT 9
US-09-236-468A-11
; Sequence 11, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:

```

9 JUL 69

US-09-236-468A-11
; Sequence 11, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:

```
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-11

Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 KYLWGFILGWGFPAAFAVAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILF 333
DB 1 KYLWGFILGWGFPAAFAVAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILF 60

RESULT 10
US-09-236-468A-15
; Sequence 15, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-15

Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 60 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTW 119
DB 1 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTW 60

RESULT 11
US-09-236-468A-19
; Sequence 19, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-19
```

```
Query Match      11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 137 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSMRLRATSI FV 196
DB 1 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSMRLRATSI FV 60

RESULT 12
US-08-468-011A-23
; Sequence 23, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-23

Query Match      10.9%; Score 59; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 387 TGLGWEIRHMCLEFNSFGFFVSIICYCNGEYQAEVKKWSRWNLSDVWKRTPPCGS 445
DB 1 TGLGWEIRHMCLEFNSFGFFVSIICYCNGEYQAEVKKWSRWNLSDVWKRTPPCGS 59

RESULT 13
US-09-236-468A-23
; Sequence 23, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
```


; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-23

Query Match 10.9%; Score 59; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 0;

Qy 387 TGLGWEIRMCHELFNFNSFQGFVSIICYNGEYQAEVKKWSEWNLSDVKRTPPCGS 445
Db 1 TGLGWEIRMCHELFNFNSFQGFVSIICYNGEYQAEVKKWSEWNLSDVKRTPPCGS 59

RESULT 14
US-09-236-468A-13
; Sequence 13, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236.468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-13

Query Match 9.6%; Score 52; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-41; Indels 0; Gaps 0;
Matches 52; Conservative 0; Mismatches 0;

Qy 334 LNTVRVLATKIWETNAVGHDTKQYRKLAETLVLVFGVHYIVFVCLPHS 385
Db 1 LNTVRVLATKIWETNAVGHDTKQYRKLAETLVLVFGVHYIVFVCLPHS 52

RESULT 15
US-08-468-011A-25
; Sequence 25, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0;

Qy 24 AQLDSGTTTIERQIVLVKAKVQCELNITAQLOEGE 60
Db 1 AQLDSGTTTIERQIVLVKAKVQCELNITAQLOEGE 37

RESULT 16
US-09-236-468A-25
; Sequence 25, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236.468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR FILING DATE: 08/468,011
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-25

Query Match 6.8%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0;

Qy 24 AQLDSGTTTIERQIVLVKAKVQCELNITAQLOEGE 60
Db 1 AQLDSGTTTIERQIVLVKAKVQCELNITAQLOEGE 37

RESULT 17
US-08-468-011A-13
; Sequence 13, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland

```

; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; OPERATING SYSTEM: IBM PS/2
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-13

Query Match          6.8%; Score 37; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 LNTVRVLATKIWETNAVGHDTRKQYKRLAKSTLVLVL 370
DB 1 LNTVRVLATKIWETNAVGHDTRKQYKRLAKSTLVLVL 37

RESULT 18
US-09-449-632-5
; Sequence 5, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Ruben, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: zebrafish
; US-09-449-632-5

Query Match          5.0%; Score 27; DB 4; Length 575;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRRLHCTRNVIHMHFLFVSFMLRA 191
DB 193 IIGYFRRLHCTRNVIHMHFLFVSFMLRA 219

RESULT 19
US-08-468-011A-20
; Sequence 20, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
```

```

; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-20

Query Match          4.6%; Score 25; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNVIHMHFLFVSFMLRA 191
DB 31 GYFRRLHCTRNVIHMHFLFVSFMLRA 55

RESULT 20
US-09-236-468A-20
; Sequence 20, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Didelphis virginiana
; US-09-236-468A-20

Query Match          4.6%; Score 25; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNVIHMHFLFVSFMLRA 191
DB 31 GYFRRLHCTRNVIHMHFLFVSFMLRA 55
```

RESULT 21
US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18
Query Match 4.6%; Score 25; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 2.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLHCTRNTHMLFVSFMLRA 191
Db 207 GYFRRLHCTRNTHMLFVSFMLRA 231
RESULT 22
US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Didelphis virginiana
US-08-142-439A-6
Query Match 4.6%; Score 25; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLHCTRNTHMLFVSFMLRA 191
Db 207 GYFRRLHCTRNTHMLFVSFMLRA 231
RESULT 23
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
; US-08-142-551B-125

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLLHCTRNYYHMLFVSFMLRA 191
|||||
Db 207 GYFRRLLHCTRNYYHMLFVSFMLRA 231

RESULT 24

US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123

; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-869-477-6

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 167 GYFRRLLHCTRNYYHMLFVSFMLRA 191
|||||
Db 207 GYFRRLLHCTRNYYHMLFVSFMLRA 231

RESULT 25

US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-19

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYIHMHFLVSEMLRA 191
Db 207 GYFRLHCTRYIHMHFLVSEMLRA 231

RESULT 26

US-08-468-011A-21
; Sequence 21, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Vi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: HLTGD74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Oistein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/468,011A
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-21

Query Match 3.9%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVAHIGVKELESIMQD 217
Db 1 KDRVVAHIGVKELESIMQD 21

RESULT 27

US-09-236-468A-21
; Sequence 21, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTGD74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21

; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-21

Query Match 3.9%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVAHIGVKELESIMQD 217
Db 1 KDRVVAHIGVKELESIMQD 21

RESULT 28

US-08-142-439A-5
; Sequence 5, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/142,439A
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
US-08-142-439A-5

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYIHMHFLVSE 187
Db 167 FRLHCTRYIHMHFLVSE 185

RESULT 29
US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCES/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
US-08-869-477-5

Query Match 3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNHYHMLFVSF 187
DB 167 FRLHCTRNHYHMLFVSF 185

RESULT 30
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof

FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-2

Query Match 3.3%; Score 18; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNHYHMLF 184
DB 167 GYFRRLHCTRNHYHMLF 184

RESULT 31
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al.; Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCES/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-20

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVRLGLYLH 262

```
Db      290 YFLATNYWILVEGLYH 307
|||||
RESULT 32
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-21

Query Match      3.3%; Score 18; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 YFLATNYWILVEGLYH 262
|||||
Db      290 YFLATNYWILVEGLYH 307
|||||
RESULT 33
US-07-864-475A-7
; Sequence 7, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-864-475A-7

Query Match      2.6%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 YFLATNYWILVEG 258
|||||
Db      6 YFLATNYWILVEG 19
|||||
RESULT 34
US-08-468-249A-7
; Sequence 7, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-249A-7

Query Match 2.6%; Score 14; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEG 258
DB 6 YFLATNYWILVEG 19

RESULT 35
US-08-468-011A-10
Sequence 10, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PP201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-10

Query Match 2.6%; Score 14; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 249 TNYWILVEGLYLH 262
DB 36 TNYWILVEGLYLH 49

RESULT 36
US-09-236-468A-10
Sequence 10, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 60
TYPE: PRT
ORGANISM: Didelphis virginiana
US-09-236-468A-10

Query Match 2.6%; Score 14; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 TNYWILVEGLYLH 262
DB 36 TNYWILVEGLYLH 49

RESULT 37
US-08-112-817C-2
Sequence 2, Application US/08112817C
Patent No. 5573928
GENERAL INFORMATION:
APPLICANT: Hsiung, Hansen M.
APPLICANT: Smith, Dennis P.
APPLICANT: Zhang, Xing-Yue
TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh IIGx compatible
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word for Macintosh v.5.1a
CURRENT APPLICATION DATA:
FILING DATE: US/08/112,817C
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Richard B.
REGISTRATION NUMBER: 35,296
REFERENCE/DOCKET NUMBER: X-9293
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3589
TELEFAX: 317-276-1294
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-817C-2

Query Match 2.4%; Score 13; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHMLF 184
|||||
Db 171 LHCTRYIHMLF 183

RESULT 38

US-08-811-897A-56
; Sequence 56, Application US/08811897A
; Patent No. 5858787

GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 5858787io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811.897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-811-897A-56

Query Match 2.4%; Score 13; DB 2; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHMLF 184
|||||

Db 173 LHCTRYIHMLF 185

RESULT 39

US-09-201-474-56
; Sequence 56, Application US/09201474
; Patent No. 6399316

GENERAL INFORMATION:

; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 6399316io
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,474
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/811,897
; FILING DATE: 05-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-201-474-56

Query Match 2.4%; Score 13; DB 4; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHMLF 184
|||||

Db 173 LHCTRYIHMLF 185

RESULT 40

US-09-414-189-1

; Sequence 1, Application US/09414189
; Patent No. 6410508
; GENERAL INFORMATION:
; APPLICANT: Isales, Carlos M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Rasmussen, Howard

```
; TITLE OF INVENTION: Glucose-dependent Insulinotropic Peptide for Use as an
; FILE REFERENCE: MCG 108
; CURRENT APPLICATION NUMBER: US/09/414,189
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: From 6-25 synthetic oligopeptide region used to
; OTHER INFORMATION: make antibodies blocking GIP receptor activation
US-09-414-189-1

Query Match          2.2%; Score 12; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
Db 141 FRLHCTRNVIH 152
|||||

RESULT 41
US-09-449-632-4
; Sequence 4, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-4

Query Match          2.0%; Score 11; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262
Db 236 YWILVEGLYLH 246
|||||

RESULT 42
US-08-468-011A-17
; Sequence 17, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; FILE REFERENCE: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESS: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
```

```
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-17

Query Match          1.8%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129
Db 1 ANYSDCLRFL 10
|||||

RESULT 43
US-09-236-468A-17
; Sequence 17, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-17

Query Match          1.8%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129
Db 1 ANYSDCLRFL 10
|||||

RESULT 44
US-08-453-956-18
; Sequence 18, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,956
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-956-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 99 LVEGLYLHNL 108

RESULT 45
US-08-631-18
Sequence 18, Application US/08086631
Patent No. 5776725
GENERAL INFORMATION:
APPLICANT: Kindvogel, Wayne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-086-631-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 99 LVEGLYLHNL 108

RESULT 46
US-08-452-930-18
Sequence 18, Application US/08452930
Patent No. 5919635
GENERAL INFORMATION:
APPLICANT: Kindvogel, Wayne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,930
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-930-18

Query Match 1.8%; Score 10; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 99 LVEGLYLHNL 108

RESULT 47
PCT-US93-08174-18
; Sequence 18, Application PC/TUS9308174
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: NAME: ZymoGenetics, Inc.
; APPLICANT: STREET: 4225 Roosevelt Way North East
; APPLICANT: CITY: Seattle, Washington
; APPLICANT: COUNTRY: United States
; APPLICANT: POSTAL CODE: 98105
; APPLICANT: TELEPHONE: (206) 547-80808
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08174
; FILING DATE: 30-AUG-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-08174-18
Query Match 1.8%; Score 10; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 255 LVEGLYHLNL 264
DB 99 LVEGLYHLNL 108
RESULT 48
US-08-845-546-10
; Sequence 10, Application US/08845546
; Patent No. 6077949
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald
; APPLICANT: Gupta, Ashwani
; APPLICANT: Vyas, Tejpal
; APPLICANT: McCallum, Kirk
; APPLICANT: Pan, Ermei
; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,546
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8607-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-845-546-10
Query Match 1.8%; Score 10; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNVIHM 181
DB 20 LHCTRNVIHM 29
RESULT 49
US-08-453-956-25
; Sequence 25, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,956
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

Search completed: December 9, 2003, 09:03:13
Job time : 23 secs

; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-956-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

RESULT 50
US-08-086-631-25
; Sequence 25 Application US/08086631
; Patent No. 5776725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,631
; FILING DATE: July 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-086-631-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 09:02:11 ; Search time 37 Seconds
(without alignments)
2719.383 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 541
Sequence: 1 MAWLGLASLHWGMLGSL.....DDILMEKPSRPMESNPDTEG 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 684280 seqs, 185983659 residues

Word size : 0

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	15	US-10-225-567A-227
2	262	48.4	550	12	US-09-826-509-565
3	216	39.9	550	15	US-10-014-162-110
4	33	6.1	546	15	US-10-014-162-109
5	27	5.0	575	12	US-10-372-095-5
6	25	4.6	515	12	US-10-267-730-18
7	25	4.6	585	12	US-10-267-730-19
8	20	3.7	20	15	US-10-225-567A-1225
9	19	3.5	353	12	US-10-017-161-696
10	19	3.5	440	12	US-09-826-509-567
11	19	3.5	440	15	US-10-225-567A-310
12	18	3.3	18	15	US-10-225-567A-1224
13	18	3.3	536	12	US-10-372-095-2
14	18	3.3	591	10	US-09-943-446-7
15	18	3.3	591	10	US-09-943-446-8

16	18	3.3	591	12	US-10-267-730-20	Sequence 20, Appl
17	18	3.3	593	10	US-09-943-446-9	Sequence 9, Appl
18	18	3.3	593	12	US-10-267-730-21	Sequence 21, Appl
19	18	3.3	593	12	US-09-826-509-563	Sequence 563, App
20	18	3.3	593	15	US-10-225-567A-229	Sequence 229, App
21	18	3.3	595	10	US-09-943-446-6	Sequence 6, Appl
22	18	3.3	594	12	US-10-017-161-710	Sequence 7, Appl
23	14	2.6	19	12	US-10-267-730-7	Sequence 7, Appl
24	13	2.4	457	12	US-09-826-509-579	Sequence 579, App
25	13	2.4	457	15	US-10-225-567A-469	Sequence 469, App
26	13	2.4	1324	9	US-09-935-371-56	Sequence 56, Appl
27	12	2.2	268	10	US-09-796-338A-19	Sequence 19, Appl
28	12	2.2	268	12	US-10-145-586-19	Sequence 19, Appl
29	12	2.2	268	12	US-10-407-079-95	Sequence 95, Appl
30	12	2.2	268	15	US-10-282-837-19	Sequence 19, Appl
31	12	2.2	271	9	US-09-795-693-36	Sequence 36, Appl
32	12	2.2	271	15	US-10-156-239-36	Sequence 36, Appl
33	12	2.2	271	15	US-10-199-485-36	Sequence 36, Appl
34	12	2.2	466	12	US-10-241-220-78	Sequence 78, Appl
35	12	2.2	466	12	US-09-826-509-507	Sequence 507, App
36	12	2.2	466	15	US-10-225-567A-128	Sequence 128, App
37	11	2.0	542	12	US-10-372-095-4	Sequence 4, Appl
38	10	1.8	11	10	US-09-966-871-62	Sequence 62, Appl
39	10	1.8	11	14	US-10-039-645-62	Sequence 62, Appl
40	10	1.8	11	15	US-10-139-084-62	Sequence 62, Appl
41	10	1.8	273	15	US-10-120-604-11	Sequence 11, Appl
42	10	1.8	477	14	US-10-010-065-6	Sequence 6, Appl
43	10	1.8	477	15	US-10-225-567A-134	Sequence 134, App
44	10	1.8	553	15	US-10-225-567A-520	Sequence 520, App
45	9	1.7	10	10	US-09-966-871-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-227
; Sequence 227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 67.1%; Score 363; DB 15; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	4	LGASLHWGMLGSLARALQSDGTTTIEEQIVLVKAKVQCELNITAQEGHGNC	63
DB	4	LGASLHWGMLGSLARALQSDGTTTIEEQIVLVKAKVQCELNITAQEGHGNC	63
QY	64	FPFWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTWDFMHSINKTWNYS	123
DB	64	FPFWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTWDFMHSINKTWNYS	123
QY	124	DCLRFLQPDISIGHQKQECERLYVMYTVGYSTISFGSLAVAILIIGYFRHLCTRNYHML	183
DB	124	DCLRFLQPDISIGHQKQECERLYVMYTVGYSTISFGSLAVAILIIGYFRHLCTRNYHML	183

; LENGTH: 546
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(546)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match 6.1%; Score 33; DB 15; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.3e-24;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGYSISFGSLAVAILIIGYFRLHCTRNHYH 180
Db 146 YTVGYSISFGSLAVAILIIGYFRLHCTRNHYH 178

RESULT 5

US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5

Query Match 5.0%; Score 27; DB 12; Length 575;
Best Local Similarity 100.0%; Pred. No. 8.3e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRLHCTRNHYHMLFVFSFMLRA 191
Db 193 IIGYFRLHCTRNHYHMLFVFSFMLRA 219

RESULT 6

US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea

US-10-267-730-18

Query Match 4.6%; Score 25; DB 12; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNHYHMLFVFSFMLRA 191
Db 207 GYFRLHCTRNHYHMLFVFSFMLRA 231

RESULT 7

US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 4.6%; Score 25; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNHYHMLFVFSFMLRA 191
Db 207 GYFRLHCTRNHYHMLFVFSFMLRA 231

RESULT 8

US-10-225-567A-1225
; Sequence 1225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenma C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1225
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1225

Query Match 3.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 ESLIMQDDPQNSTEATSVDK 230

Db 1 ESLIMQDDPNSIATSVDK 20
|||||

RESULT 9

US-10-017-161-696
; Sequence 696, Application US/10017161
; Publication No. US20030143668A1

; GENERAL INFORMATION:

; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI

; APPLICANT: AKIYAMA, YUTAKA

; APPLICANT: ASURATANI, HIROYUKI

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 084335/0152

; CURRENT APPLICATION NUMBER: US/10/017,161

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: JP 2001/246789

; PRIOR FILING DATE: 2001-06-18

; NUMBER OF SEQ ID NOS: 2430

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 696

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-017-161-696

Query Match

Best Local Similarity 3.5%; Score 19; DB 12; Length 353;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYIHMLFVSF 187

Db 23 FRLHCTRNYIHMLFVSF 41
|||||

RESULT 10

US-09-826-509-567

; Sequence 567, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruntsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 567

; LENGTH: 440

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-567

Query Match

Best Local Similarity 3.5%; Score 19; DB 12; Length 440;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYIHMLFVSF 187

Db 167 FRLHCTRNYIHMLFVSF 185
|||||

RESULT 11

US-10-225-567A-310

; Sequence 310, Application US/10225567A

; Publication No. US20030113798A1
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 310

; LENGTH: 440

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-310

Query Match

Best Local Similarity 3.5%; Score 19; DB 15; Length 440;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYIHMLFVSF 187

Db 167 FRLHCTRNYIHMLFVSF 185
|||||

RESULT 12

US-10-225-567A-1224

; Sequence 1224, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1224

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-1224

Query Match

Best Local Similarity 3.3%; Score 18; DB 15; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 KAKVQCELNITLAQLQEGE 60

Db 1 KAKVQCELNITLAQLQEGE 18
|||||

RESULT 13

US-10-372-095-2

; Sequence 2, Application US/10372095

; Publication No. US20030162256A1

; GENERAL INFORMATION:

; APPLICANT: Juppner, Harald

; APPLICANT: Rubin, David A.

; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof

; FILE REFERENCE: 0609.4740002

; CURRENT APPLICATION NUMBER: US/10/372,095

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/449,632

```
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match      3.3%; Score 18; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRHLCTRNTHMLF 184
Db 167 GYFRHLCTRNTHMLF 184

RESULT 14
US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-943-446-7

Query Match      3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
Db 290 YFLATNYWILVEGLYH 307

RESULT 15
US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591

Query Match      3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
Db 290 YFLATNYWILVEGLYH 307

RESULT 16
US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match      3.3%; Score 18; DB 12; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYH 262
Db 290 YFLATNYWILVEGLYH 307

RESULT 17
US-09-943-446-9
; Sequence 9, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-446-9

Query Match      3.3%; Score 18; DB 10; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|
Db 290 YFLATNYWILVEGLYLH 307

RESULT 18

US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 3.3%; Score 18; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|
Db 290 YFLATNYWILVEGLYLH 307

RESULT 19

US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brudnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 3.3%; Score 18; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|
Db 290 YFLATNYWILVEGLYLH 307

RESULT 20

US-10-225-567A-229
; Sequence 229, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-229

Query Match 3.3%; Score 18; DB 15; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|
Db 290 YFLATNYWILVEGLYLH 307

RESULT 21

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891A9R
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 3.3%; Score 18; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 6.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|
Db 289 YFLATNYWILVEGLYLH 306

RESULT 22

US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABEURAI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match 3.3%; Score 18; DB 12; Length 964;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWTLVVEGLYH 262
Db 564 YFLATNYWTLVVEGLYH 581

RESULT 23
US-10-267-730-7
; Sequence 7, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding; 1st to last; peptide fragment
US-10-267-730-7

Query Match 2.6%; Score 14; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWTLVVEG 258
Db 6 YFLATNYWTLVVEG 19

RESULT 24
US-09-826-509-579
; Sequence 579, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: NO. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 579
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-579

Query Match 2.4%; Score 13; DB 12; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNHYHMLF 184
Db 170 LHCTRNHYHMLF 182

RESULT 25
US-10-225-567A-469
; Sequence 469, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Glenma C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 469
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-469

Query Match 2.4%; Score 13; DB 15; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNHYHMLF 184
Db 170 LHCTRNHYHMLF 182

RESULT 26
US-09-935-371-56
; Sequence 56, Application US/09935371
; Patent No. US2002015533A1
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Tetsushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. US2002015533A1
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; FILE REFERENCE: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-935-371-56
      2.4%; Score 13; DB 10; Length 1324;
      Best Local Similarity 100.0%; Pred. No. 0.0012;
      Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNIHMLF 184
      |||||
Db 173 LHCTRYNIHMLF 185

RESULT 27
US-09-796-338A-19
; Sequence 19, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-796-338A-19
      2.2%; Score 12; DB 9; Length 268;
      Best Local Similarity 100.0%; Pred. No. 0.0028;
      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYNIH 180

RESULT 28
US-10-145-586-19
; Sequence 19, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; FILE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-19
      2.2%; Score 12; DB 12; Length 268;
      Best Local Similarity 100.0%; Pred. No. 0.0028;
      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYNIH 180
      |||||
Db 29 FRRLHCTRYNIH 40

RESULT 29
US-10-407-079-95
; Sequence 95, Application US/10407079
; Publication No. US20030215860A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 18636, 2466, 43238, 1983, 52881, 2398,
; FILE OF INVENTION: 45449, 50289, 52872 AND 26908 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0510MNM
; CURRENT APPLICATION NUMBER: US/10/407,079
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/226,102
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,041
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/225,094
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,185
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/272,417
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/715,790
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/191,845
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 10/282,837
; PRIOR FILING DATE: 2002-10-29
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,371
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,474
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-935-371-56
      2.4%; Score 13; DB 10; Length 1324;
      Best Local Similarity 100.0%; Pred. No. 0.0012;
      Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNIHMLF 184
      |||||
Db 173 LHCTRYNIHMLF 185

RESULT 27
US-09-796-338A-19
; Sequence 19, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-796-338A-19
      2.2%; Score 12; DB 9; Length 268;
      Best Local Similarity 100.0%; Pred. No. 0.0028;
      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYNIH 180
```

```
; PRIOR APPLICATION NUMBER: US 09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid consensus sequence
US-10-407-079-95

Query Match          2.2%; Score 12; DB 12; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
   |||||
Db 29 FRLHCTRNVIH 40

RESULT 30
US-10-282-837-19
; Sequence 36, Application US/10282837
; Publication No. US20030082738A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/10/282,837
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-282-837-19

Query Match          2.2%; Score 12; DB 15; Length 268;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
   |||||
Db 29 FRLHCTRNVIH 40

RESULT 31
US-09-795-693-36
; Sequence 36, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, NO. US20020068710A1 Human Transporters
; FILE REFERENCE: 35800/209292
; CURRENT APPLICATION NUMBER: US/09/795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-09-795-693-36

Query Match          2.2%; Score 12; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
   |||||
Db 29 FRLHCTRNVIH 40

RESULT 32
US-10-156-239-36
; Sequence 36, Application US/10156239
; Publication No. US20030036074A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: No. US20030036074A1 Nucleic Acid Sequences Encoding Human Tr
; TITLE OF INVENTION: Arpase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A
; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
; FILE REFERENCE: 35800/247645
; CURRENT APPLICATION NUMBER: US/10/156,239
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pfam consensus sequence
US-10-156-239-36

Query Match          2.2%; Score 12; DB 15; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
   |||||
Db 29 FRLHCTRNVIH 40

RESULT 33
US-10-199-485-36
; Sequence 36, Application US/10199485
; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
```

; TITLE OF INVENTION: 32613, No. US20030077626A1el Human Transporters
; FILE REFERENCE: 35800/249488
; CURRENT APPLICATION NUMBER: US/10/199,485
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-10-199-485-36

Query Match 2.2%; Score 12; DB 15; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHLCTRYIH 180
Db 29 FRRHLCTRYIH 40
|||||

RESULT 34
US-10-241-220-78
; Sequence 78, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 78
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-78

Query Match 2.2%; Score 12; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHLCTRYIH 180
Db 162 FRRHLCTRYIH 173
|||||

RESULT 35
US-09-826-509-507
; Sequence 507, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: ARN-207
; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 507
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-507

Query Match 2.2%; Score 12; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHLCTRYIH 180
Db 162 FRRHLCTRYIH 173
|||||

RESULT 36
US-10-225-567A-128
; Sequence 128, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-128

Query Match 2.2%; Score 12; DB 15; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRHLCTRYIH 180
Db 162 FRRHLCTRYIH 173
|||||

RESULT 37
US-10-372-095-4
; Sequence 4, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542

; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-4

Query Match 2.0%; Score 11; DB 12; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWLVVGLYH 262
DB 236 YWLVVGLYH 246

RESULT 38

US-09-966-871-62

; Sequence 62, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-62

Query Match 1.8%; Score 10; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
DB 1 TRNYIHMHLF 10

RESULT 39

US-10-039-645-62

; Sequence 62, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No. US20020147170
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-62

Query Match 1.8%; Score 10; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
|||||

Db 1 TRNYIHMHLF 10

RESULT 40

US-10-139-084-62

; Sequence 62, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Beinborn, Martin
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Dose Response-Based Methods For
; TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-62

Query Match 1.8%; Score 10; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TRNYIHMHLF 184
|||||

Db 1 TRNYIHMHLF 10

RESULT 41

US-10-120-604-11

; Sequence 11, Application US/10120604
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED REC
; TITLE OF INVENTION: HGPRTMY28 AND HGPRTMY29, AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-11

Query Match 1.8%; Score 10; DB 15; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHM 181
|||||

Db 33 LHCTRYIHM 42

RESULT 42

US-10-010-065-6

; Sequence 6, Application US/10010065

; Publication No. US20020144300A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING GLUCAGON
; TITLE OF INVENTION: RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-648
; CURRENT APPLICATION NUMBER: US/10/010.065
; CURRENT FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2001-12-05
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-065--6

Query Match 1.8%; Score 10; DB 14; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

RESULT 43

US-10-225-567A-134
; Sequence 134, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-134

Query Match 1.8%; Score 10; DB 15; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||
Db 243 LVEGLYLHNL 252

RESULT 44

US-10-225-567A-520

; Sequence 520, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 520
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-520

Query Match 1.8%; Score 10; DB 15; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNHYHM 181
|||||
Db 206 LHCTRNHYHM 215

RESULT 45

US-09-966-871-67
; Sequence 67, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:

; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871

; CURRENT FILING DATE: 2001-09-28
; PRIOR FILING DATE: 2000-09-28
; PRIOR FILING DATE: 2000-09-28
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-67

Query Match 1.7%; Score 9; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
|||||
Db 1 RNYIHMHLF 9

RESULT 46

US-10-039-645-67
; Sequence 67, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:

; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No. US2002014

; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR FILING DATE: 2001-10-25
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 10
; TYPE: PRT

/ ORGANISM: Homo sapiens
US-10-039-645-67

Query Match 1.7%; Score 9; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
Db 1 RNYIHMHLF 9

RESULT 47

US-10-139-084-67
Sequence 67, Application US/10139084
Publication No. US2003008731A1
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
FILE REFERENCE: 00398/515002
CURRENT APPLICATION NUMBER: US/10/139,084
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/288,647
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-139-084-67

Query Match 1.7%; Score 9; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 RNYIHMHLF 184
Db 1 RNYIHMHLF 9

RESULT 48

US-10-267-730-28
Sequence 28, Application US/10267730
Publication No. US20030153041A1
GENERAL INFORMATION:
APPLICANT: Segre, Gino V.
APPLICANT: Kronenberg, Henry M.
APPLICANT: Abou-Samra, Abdul-Badi
APPLICANT: Juppner, Harald
APPLICANT: Potts, Jr., John T.
APPLICANT: Schipani, Ernestina
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
FILE REFERENCE: 00786/071005
CURRENT APPLICATION NUMBER: US/10/267,730
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 08/471,494
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 18
TYPE: PRT
ORGANISM: Rattus rattus
US-10-267-730-28

Query Match 1.7%; Score 9; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 FNSFQGFV 409

Db 3 FNSFQGFV 11

RESULT 49

US-10-225-567A-1227
Sequence 1227, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Roush, Glenn C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1227
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1227

Query Match 1.7%; Score 9; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 DDILMEKPS 530
Db 12 DDILMEKPS 20

RESULT 50

US-09-935-371-7
Sequence 7, Application US/09935371
Patent No. US20020155533A1
GENERAL INFORMATION:
APPLICANT: ONDA, Haruo
OHTAKI, Tetsuya
MASUDA, Yasushi
KITADA, Chieko
ISHIBASHI, Yoshihiro
HOSOYA, Masaki
OGI, Kazuhiro
MIYAMOTO, Yasunori
HABATA, Yugo
SHIMAMOTO, No. US20020155533A1
TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
SAID PROTEIN, AND USE THEREOF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,371
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,474

;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-935-371-7

Query Match 1.7%; Score 9; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 LFVSPMLRA 191
Db 26 LFVSPMLRA 34

Search completed: December 9, 2003, 09:07:45
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:58:00 ; Search time 20 seconds
(without alignments)
2601.363 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGHSLHWGMLGSL.....DDLMEKPSRPMSNPDEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 9616882 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 76:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	550	2 A57519	parathyroid hormone
2	25	4.6	585	2 A39286	parathyroid hormone
3	19	3.5	440	2 JC2532	secretin receptor
4	19	3.5	449	2 S16319	secretin receptor
5	18	3.3	589	2 I59297	parathyroid hormone
6	18	3.3	591	2 S44203	parathyroid hormone
7	18	3.3	591	2 I54195	parathyroid hormone
8	18	3.3	593	2 A49191	parathyroid hormone
9	13	2.4	455	2 I53273	gastric inhibitory
10	13	2.4	459	2 JH0594	vasoactive intesti
11	13	2.4	460	2 JC2194	vasoactive intesti
12	13	2.4	462	2 JC2462	gastric inhibitory
13	13	2.4	495	2 JC2195	vasoactive intesti
14	12	2.2	466	2 G02234	gastric inhibitory
15	12	2.2	466	2 S66676	glucose-dependent
16	12	2.2	491	2 I37411	glucose-dependent
17	10	1.8	477	2 JC2041	glucagon receptor
18	9	1.7	381	2 S33449	pituitary adenyilat
19	9	1.7	437	2 JU0185	PACAP/VIP receptor
20	9	1.7	437	2 S39069	vasoactive intesti
21	9	1.7	438	2 G02822	vasoactive intesti
22	9	1.7	463	2 S71624	glucagon-like pept
23	9	1.7	463	2 A46172	glucagon-like pept
24	9	1.7	463	2 I84494	glucagon-like pept
25	9	1.7	467	2 JN0616	pituitary adenyilat
26	9	1.7	485	2 JQ1957	glucagon receptor
27	9	1.7	485	2 JC4363	glucagon receptor
28	9	1.7	495	2 S36114	pituitary adenyilat
29	9	1.7	495	2 S39061	pituitary adenyilat

30 9 1.7 513 2 S47631 pituitary adenyilat
31 9 1.7 523 2 S39060 pituitary adenyilat
32 9 1.7 525 2 JN0902 pituitary adenyilat
33 8 1.5 375 2 I38879 corticotropin rele
34 8 1.5 411 2 A55610 corticotropin rele
35 8 1.5 411 2 S26195 probable carboxyl-
36 8 1.5 415 2 S39535 corticotropin-rele
37 8 1.5 415 2 I58144 corticotropin-rele
38 8 1.5 430 2 A56726 corticotropin rec
39 8 1.5 431 2 I49279 corticotropin rec
40 8 1.5 431 2 I49149 CRF receptor - mou
41 8 1.5 444 2 A48260 corticotropin rec
42 8 1.5 533 1 GRBYCP cytosine/purine tr
43 8 1.5 1904 2 TL3256 tail-host specific
44 7 1.3 50 2 B37334 L-mandelate dehydr
45 7 1.3 80 2 AB2755 host factor I [imp

ALIGNMENTS

RESULT 1

A57519
parathyroid hormone receptor 2 precursor - human
N/Alternate names: PTH2 receptor
C/Species: Homo sapiens (man)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C/Accession: A57519
R/Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A/Title: Identification and functional expression of a receptor selectively recognizi
A/Reference number: A57519; MUID:95318121; PMID:7797535
A/Accession: A57519
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-350 <USD>
A/Cross-references: GB:U25128; NID:9887966; PIDN:AAC50157.1; PID:9887967
C/Genetics:
A/Gene: GDB:PTH2R; PTHR2R
A/Cross-references: GDB:731977; OMIM:601469
A/Map position: 2q33-2q33
C/Superfamily: glucagon receptor
C/Keywords: hormone receptor

Query Match 67.1%; Score 363; DB 2; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 LGASHVWGMLGSLGSLAQAQLDSGTTTIEQIVLVKAKVQCELNITAIQOEGGNC 63
DB 4 LGASHVWGMLGSLGSLAQAQLDSGTTTIEQIVLVKAKVQCELNITAIQOEGGNC 63
QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
DB 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANY 123
QY 124 DCLRLPQDTSIGKQECERLYMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIHMHL 183
DB 124 DCLRLPQDTSIGKQECERLYMYTVGYSISFGSLAVAILIIGYFRLHCTRNYIHMHL 183
QY 184 FVSPMLRATSLFVKDRVVHAGVKELESILIMQDDPNSIATSVKDSQYIGCKIAVVMF 243
DB 184 FVSPMLRATSLFVKDRVVHAGVKELESILIMQDDPNSIATSVKDSQYIGCKIAVVMF 243
QY 244 IYFLATNYTWLVEGLYHNLIFVAFSFTKYLGMGFIIGWGFPAAFVAWAVARATLAD 303
DB 244 IYFLATNYTWLVEGLYHNLIFVAFSFTKYLGMGFIIGWGFPAAFVAWAVARATLAD 303
QY 304 ARCWELSGADIKWYQAPILAAIGNIFLNTVRLVATKIWTETNAVGHDTKQYRKLAK 363
DB 304 ARCWELSGADIKWYQAPILAAIGNIFLNTVRLVATKIWTETNAVGHDTKQYRKLAK 363
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWEIRMHCELFNSPQGFVSIYCYCNGEVAE 423

Db 364 STLVVLVFGVHIVFVCLPHSTGLGWEIRMCHELFNFSSQFFVSIYCYCNGEVOAE 423
 QY 424 VKQWMSRWNLSDVWKRTTPPGSGRRCGSVLTITVTHSTSSQSQVAA 467
 Db 424 VKQWMSRWNLSDVWKRTTPPGSGRRCGSVLTITVTHSTSSQSQVAA 467

RESULT 2

A39286
 parathyroid hormone / parathyroid hormone-related peptide - North American opossum
 C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 11-Jan-2000
 C:Accession: A39286
 R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K
 Science 254, 1024-1026, 1991
 A:Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
 A:Reference number: A39286; MUID:92054592; PMID:1658941
 A:Accession: A39286
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-585 <JUE>
 A:Cross-references: GB:M74445
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.8%; Score 25; DB 2; Length 585;
 Best Local Similarity 100.0%; Pred. No. 6.5e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNYIHMLFVSEMLRA 191
 Db 207 GYFRRLHCTRNYIHMLFVSEMLRA 231

RESULT 3

JC2532
 secretin receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
 C:Accession: JC2532
 R:Jiang, S.; Ulrich, C.
 Biochem. Biophys. Res. Commun. 207, 883-890, 1995
 A:Title: Molecular cloning and functional expression of a human pancreatic secretin rece
 A:Reference number: JC2532; MUID:95169147; PMID:7864894
 A:Accession: JC2532
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-440 <JIA>
 A:Cross-references: EMBL:U20178; NID:9662795; PIDN:AAC50106.1; PID:9662796
 A:Experimental source: pancreas
 C:Genetics:
 A:Gene: GDB:SCTR
 A:Cross-references: GDB:270546; OMIM:182098
 A:Map position: 2q14.1-2q14.1
 C:Superfamily: glucagon receptor

Query Match 3.5%; Score 19; DB 2; Length 440;
 Best Local Similarity 100.0%; Pred. No. 7e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNYIHMLFVVSF 187
 Db 167 FRRLHCTRNYIHMLFVVSF 185

RESULT 4

S16319
 secretin receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S16319
 R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.

EMBO J. 10, 1635-1641, 1991
 A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
 A:Reference number: S16319; MUID:91266890; PMID:1646711
 A:Accession: S16319
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-449 <ISH>
 A:Cross-references: EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.5%; Score 19; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 7.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNYIHMLFVVSF 187
 Db 167 FRRLHCTRNYIHMLFVVSF 185

RESULT 5

I59297
 parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I59297
 R:McCuaiig, K.A.; Clarke, J.C.; White, J.H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
 A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parath
 A:Reference number: I59297; MUID:94255468; PMID:8197183
 A:Accession: I59297
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-589 <RES>
 A:Cross-references: GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151
 C:Genetics:
 A:Gene: PTHR
 A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2
 C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 589;
 Best Local Similarity 100.0%; Pred. No. 9.4e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 6

S44203
 parathyroid hormone-related peptide receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
 C:Accession: S44203
 R:Kaprelian, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boo
 submitted to the EMBL Data Library, April 1994
 A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related
 A:Reference number: S44203
 A:Accession: S44203
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-591 <KAR>
 A:Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
 C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 9.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 Db 290 YFLATNYWILVEGLYLH 307

RESULT 7
I54195

parathyroid hormone/parathyroid hormone related-peptide receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
 C:Accession: I54195; A42698
 R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, M.; Rivier
 Genomics 20, 20-26, 1994
 A:Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
 and rat genomes.

A:Reference number: I54195; MUID:94292182; PMID:8020952

A:Accession: I54195

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-591 <RES>

A:CROSS-references: GB:I19475; NID:9467316; PIDN:AA468098.1; PID:9467317
 R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
 Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992

A:Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
 n of both cAMP and inositol triphosphates and increases intracellular free calcium.

A:Reference number: A42698; MUID:92212903; PMID:1313566

A:Accession: A42698

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-585, 'G', 587-591 <ABO>

A:Experimental source: ROS 17/2.8 osteosarcoma cells

A>Note: sequence extracted from NCBI backbone (NCBIP:92187)

C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;

Best Local Similarity 100.0%; Pred. No. 9.5e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262

|||||

Db 290 YFLATNYWILVEGLYLH 307

RESULT 8

A49191

parathyroid hormone/PTH-related peptide receptor - human

N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000

C:Accession: I38139; A49191; I38113; G01562; S29610

R:Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.
 Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Juppner, H.

J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995

A:Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons

A:Reference number: I38139; MUID:95263723; PMID:7745008

A:Accession: I38139

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-593 <RES>

A:CROSS-references: EMBL:U22409; NID:9897594; PIDN:AA860657.1; PID:9897596

R:Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.

Endocrinology 132, 2157-2165, 1993

A:Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa

A:Reference number: A49191; MUID:93238641; PMID:8386612

A:Accession: A49191

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-593 <SCH>

A:CROSS-references: GB:I04308; NID:9190721; PIDN:AAA36525.1; PID:9190722

A>Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
 R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.
 Eur. J. Pharmacol. 246, 149-155, 1993

A:Title: Cloning and functional expression of a human parathyroid hormone receptor.

A:Reference number: I38113; MUID:93387403; PMID:8397094

A:Accession: I38113

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-593 <RE2>

A:CROSS-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813

R:Levine, M.

submitted to the EMBL Data Library, November 1994

A:Reference number: G07787

A:Accession: G01562

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-593 <LEV>

A:CROSS-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130

C:Genetics:

A:introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;

C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.3%; Score 18; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 9.5e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262

|||||

Db 290 YFLATNYWILVEGLYLH 307

RESULT 9

I53273

gastric inhibitory polypeptide receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999

C:Accession: I53273

R:Usdin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.

Endocrinology 133, 2861-2870, 1993

A:Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive

A:Reference number: I53273; MUID:94062667; PMID:8243312

A:Accession: I53273

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-455 <RES>

A:CROSS-references: GB:I19660; NID:g431448; PIDN:AAC37637.1; PID:g431449

C:Superfamily: glucagon receptor

Query Match 2.4%; Score 13; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 9.8e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRLHCTRYIHM 181

|||||

Db 159 FRRLHCTRYIHM 171

RESULT 10

JH0594

vasoactive intestinal peptide receptor precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: JH0594; S56014

R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.

Neuron 8, 811-819, 1992

A:Title: Functional expression and tissue distribution of a novel receptor for vasoac

A:Reference number: JH0594; MUID:92232309; PMID:1314625

A:Accession: JH0594

A:Molecule type: mRNA

A:Residues: 1-459 <ISH>

A:CROSS-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641

A:Experimental source: lung

R:Fei, L.; Melmed, S.

Biochem. J. 308, 719-723, 1995

A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene

A:Reference number: S56014; MUID:97104266; PMID:8948424

A:Accession: S56014

A>Status: preliminary; translation not shown

A:Molecule type: DNA

```

A;Residues: 1-26 <PBI>
A;Cross-references: EMBL:U10635; NID:g505752; PIDN:AA848185.1; PID:g514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 2.4%; Score 13; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNIIHMLF 184
Db 171 LHCTRNIIHMLF 183
RESULT 11
JC2194
vasoactive intestinal peptide receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: JC2194; JN0604; PC2289; S38397
R;Couvineau, A.; Ruyver-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA ex
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2194
A;Molecule type: mRNA
A;Residues: 1-460 <COU>
A;Cross-references: EMBL:X75299; NID:g407461; PIDN:CAA53046.1; PID:g407462
A;Experimental source: jejunal epithelial cell; clone hIVR8
R;Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A;Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin
A;Reference number: JN0604; MUID:93290641; PMID:8390245
A;Accession: JN0604
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-284,288-460 <SRE>
A;Cross-references: GB:LI3288; NID:g292903; PIDN:AAA36805.1; PID:g292904
R;Couvineau, A.; Gaudin, P.; Maoret, J.J.; Ruyver-Fessard, C.; Nicole, P.; Laburthe, M.
Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A;Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A;Reference number: PC2289; MUID:95118345; PMID:7818527
A;Accession: PC2289
A;Molecule type: mRNA
A;Residues: 63-129 <CO2>
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVR1
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pro
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-194/Domain: transmembrane #status predicted <TM2>
F;216-234/Domain: transmembrane #status predicted <TM3>
F;258-277/Domain: transmembrane #status predicted <TM4>
F;299-319/Domain: transmembrane #status predicted <TM5>
F;346-363/Domain: transmembrane #status predicted <TM6>
F;377-396/Domain: transmembrane #status predicted <TM7>
F;58,69,100,293/Binding site: carboxylate (Asn) (covalent) #status predicted
F;76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
Query Match 2.4%; Score 13; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 172 LHCTRNIIHMLF 184
Db 170 LHCTRNIIHMLF 182
RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N;Alternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic isle
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:g644880; PIDN:BA07284.1; PID:g765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>
Query Match 2.4%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 FRRLHCTRNIIHMLF 181
Db 159 FRRLHCTRNIIHMLF 171
RESULT 13
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone hIVR5) - hume
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; S42087
R;Couvineau, A.; Ruyver-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-D
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDN
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2195
A;Molecule type: mRNA
A;Residues: 1-495 <COU>
A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAA54814.1; PID:g456353
A;Experimental source: jejunal epithelial cell
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVR1
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status pre
F;180-203/Domain: transmembrane #status predicted <TM1>
F;211-229/Domain: transmembrane #status predicted <TM2>
F;251-269/Domain: transmembrane #status predicted <TM3>
F;290-312/Domain: transmembrane #status predicted <TM4>
F;334-354/Domain: transmembrane #status predicted <TM5>

```

F:381-398/Domain: transmembrane #status predicted <TM6>
 F:412-431/Domain: transmembrane #status predicted <TM7>
 F:93,104,135,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
 F:285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
 F:485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNHMLF 184
 |||||
 Db 205 LHCTRYNHMLF 217

RESULT 14

G02234

gastric inhibitory polypeptide receptor - human

N:Alternate names: GIP receptor

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C:Accession: G02234

R:Bornier, T.I.; Usdin, T.B.

submitted to the EMBL Data Library, October 1995

A:Reference number: G09336

A:Accession: G02234

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-466 <BON>

A:Cross-references: EMBL:U39231; NID:G1066050; PIDN:AA84418.1; PID:G1066051

C:Genetics:

A:Gene: GDB:GIPR

A:Cross-references: GDB:335023

A:Map position: 19q13.3-19q13.3

C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNH 180
 |||||
 Db 162 FRLHCTRYNH 173

RESULT 15

S66676

glucose-dependent insulinotropic protein receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S66676

R:Volz, A.; Goetze, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goetze, B.

FEBS Lett. 373, 23-29, 1995

A:Title: Molecular cloning, functional expression, and signal transduction of the GIP-re

A:Reference number: S66676; MUID:96013879; PMID:7589426

A:Accession: S66676

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-466 <VOL>

A:Cross-references: GB:S79852

A:Note: the authors translated the codon GCC for residue 427 as Leu

C:Superfamily: glucagon receptor

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-466/Product: Glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.2%; Score 12; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNH 180
 |||||
 Db 162 FRLHCTRYNH 173

RESULT 16

I37411

glucose-dependent insulinotropic polypeptide receptor - human

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999

C:Accession: I37411

R:Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens

Diabetes 44, 1202-1208, 1995

A:Title: Cloning, functional expression, and chromosomal localization of the human pa

A:Reference number: I37411; MUID:96007224; PMID:7556958

A:Accession: I37411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-491 <RES>

A:Cross-references: EMBL:X81832; NID:G1030050; PIDN:CAA57426.1; PID:G1030051

C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNH 180
 |||||
 Db 161 FRLHCTRYNH 172

RESULT 17

JC2041

glucagon receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999

C:Accession: JC2041

R:MacNeil, D.J.; Occhi, J.L.; Hey, P.J.; Strader, C.D.; Graziano, M.P.

Biochem. Biophys. Res. Commun. 198, 328-334, 1994

A:Title: Cloning and expression of a human glucagon receptor.

A:Reference number: JC2041; MUID:94121651; PMID:7507321

A:Accession: JC2041

A:Molecule type: mRNA

A:Residues: 1-477 <MAC>

A:Cross-references: GB:U03469; NID:9439689; PIDN:AAC52063.1; PID:9439690

C:Genetics:

A:Gene: GDB:GGR; GGR

A:Cross-references: GDB:304516; OMIM:138033

A:Map position: 17q25-17q25

C:Superfamily: glucagon receptor

C:Keywords: glycoprotein; receptor; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-477/Product: glucagon receptor #status predicted <MAT>

F:143-166/Domain: transmembrane #status predicted <TM1>

F:174-194/Domain: transmembrane #status predicted <TM2>

F:226-244/Domain: transmembrane #status predicted <TM3>

F:266-285/Domain: transmembrane #status predicted <TM4>

F:302-323/Domain: transmembrane #status predicted <TM5>

F:352-369/Domain: transmembrane #status predicted <TM6>

F:386-403/Domain: transmembrane #status predicted <TM7>

F:46,59,74,78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.8%; Score 10; DB 2; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
 |||||
 Db 243 LVEGLYLHNL 252

RESULT 18

S33449

pituitary adenylylate cyclase-activating polypeptide receptor homolog - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C:Accession: S33449
 R: Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Christophe, J.
 submitted to the EMBL Data Library, May 1993
 A:Description: Molecular cloning of a PACAP-type receptor.
 A:Reference number: S33449
 A:Accession: S33449
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-381 <SVO>
 A:Cross-references: EMBL:222735; NID:g311228; PIDN:CAA80429.1; PID:g311229
 C:Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSEMLRA 191
 |||||
 Db 77 LFVSEMLRA 85

RESULT 19

JU0185
 PACAP/VIP receptor (PACAPR-3) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
 C:Accession: A53471; JU0185
 R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;
 Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994
 A:Title: Cloning and functional characterization of a third pituitary adenylate cyclase-
 A:Reference number: A53471; MUID:94195806; PMID:8146174
 A:Accession: A53471
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-437 <RES>
 A:Cross-references: GB:D28132; NID:g473721; PIDN:BAA05674.1; PID:g496376
 A:Experimental source: strain C57BL/6
 C:Superfamily: glucagon receptor
 C:Keywords: receptor

Query Match 1.7%; Score 9; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 153 LHCTRNYYIH 161

RESULT 20

S39069
 vasoactive intestinal peptide receptor VIP2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S39069
 R:Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.
 FEBS Lett. 334, 3-8, 1993
 A:Title: The Vip(2) receptor: molecular characterization of a cDNA encoding a novel recep
 A:Reference number: S39069; MUID:94039806; PMID:8224221
 A:Accession: S39069
 A:Molecule type: mRNA
 A:Residues: 1-437 <LUT>
 A:Cross-references: EMBL:225885; NID:g414188; PIDN:CAA81104.1; PID:g414189
 C:Superfamily: glucagon receptor
 C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 153 LHCTRNYYIH 161

RESULT 21

G02822
 vasoactive intestinal peptide receptor 2 - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000
 C:Accession: G02822; JC2463
 R:Lutz, E.M.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01736
 A:Accession: G02822
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-438 <LUT>
 A:Cross-references: EMBL:X95097; NID:g1160469; PIDN:CAA64474.1; PID:g1160470
 R:Svoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr
 Biochem. Biophys. Res. Commun. 205, 1617-1624, 1994
 A:Title: Molecular cloning and functional characterization of a human VIP receptor fr
 A:Reference number: JC2463; MUID:95110300; PMID:7811244
 A:Accession: JC2463
 A:Molecule type: mRNA
 A:Residues: 1-38, 'T', '40-411, 'H', '413-423, 'A', '425-438 <SVO>
 A:Cross-references: GB:L36566; NID:g550477; PIDN:AAC37569.1; PID:g550478
 A:Experimental source: SUP-T1 lymphoblast cell line
 C:Genetics:

A:Gene: GDB:VIPR2
 A:Cross-references: GDB:335025
 A:Map position: 7q36.3-7q36.3
 C:Superfamily: glucagon receptor
 C:Keywords: glycoprotein; intestine; receptor; transmembrane protein
 F:130-150/Domain: transmembrane #status predicted <TM1>
 F:160-179/Domain: transmembrane #status predicted <TM2>
 F:206-228/Domain: transmembrane #status predicted <TM3>
 F:241-262/Domain: transmembrane #status predicted <TM4>
 F:282-304/Domain: transmembrane #status predicted <TM5>
 F:329-349/Domain: transmembrane #status predicted <TM6>
 F:361-384/Domain: transmembrane #status predicted <TM7>
 F:58,88,92/Binding site: carbohydrate (Asn) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 438;
 Best Local Similarity 100.0%; Pred. No. 1-2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYIH 180
 |||||
 Db 154 LHCTRNYYIH 162

RESULT 22

S71624
 Glucagon-like peptide-1 receptor, pancreatic - human
 N:Alternate names: GLP-1-receptor
 C:Species: Homo sapiens (man)
 C:Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000
 C:Accession: S71624; JN0807; I38398; I84485; S45707
 R:Wei, Y.; Mojsov, S.
 FEBS Lett. 358, 219-224, 1995
 A:Title: Tissue-specific expression of the human receptor for glucagon-like peptide-1
 A:Reference number: S71624; MUID:95145713; PMID:7843404
 A:Accession: S71624
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-463 <WEI>
 A:Cross-references: EMBL:U10037; NID:g717033; PIDN:AAA63787.1; PID:g717034
 R:Graziano, M.P.; Hey, P.J.; Borkowski, D.; Chicchi, G.G.; Strader, C.D.
 Biochem. Biophys. Res. Commun. 196, 141-146, 1993
 A:Title: Cloning and functional expression of a human glucagon-like peptide-1 recept
 A:Reference number: JN0807; MUID:94029985; PMID:8216285
 A:Accession: JN0807
 A:Molecule type: mRNA
 A:Residues: 1-220, 'Q', '222-463 <GRA>

A;Cross-references: GB:I23503; NID:q402480; PIDN:AAAL7021.1; PID:g402481
 A;Experimental source: gastric tumor cell
 R;Dillon, J.S.; Tanizawa, Y.; Wheeler, M.B.; Leng, X.H.; Ligon, B.B.; Rabin, D.U.; Yoo-W
 Endocrinology 133, 1907-1910, 1993
 A;Title: Cloning and functional expression of the human glucagon-like peptide-1 (GLP-1)
 A;Reference number: I38398; MUID:94008746; PMID:8404634
 A;Accession: I38398
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-220, 'Q', 222-259, 'F', 261-315, 'G', 317-463 <RES>
 A;Cross-references: EMBL:U01157; NID:9684918; PIDN:AAA62471.1; PID:g393108
 A;Accession: I84485
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-220, 'Q', 222-259, 'F', 261-315, 'G', 317-463 <RE2>
 A;Cross-references: EMBL:U01156; NID:g393105; PIDN:AA50050.1; PID:g393106
 R;van Eyll, B.; Lankat-Buttgeit, B.; Bode, H.P.; Goetze, R.; Goetze, B.
 FEBS Lett. 348, 7-13, 1994
 A;Title: Signal transduction of the GLP-1-receptor cloned from a human insulinoma.
 A;Reference number: S45707; MUID:94298957; PMID:7517895
 A;Accession: S45707
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-11, 'V', 13-136, 'R', 138-220, 'Q', 222-259, 'F', 261-463 <BYL>
 C;Comment: This protein acts the stimulation of adenylyl cyclase to raise intracellular
 C;Function:
 A;Description: stimulates glucose-induced insulin secretion
 C;Superfamily: Glucagon receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; pancreas; transmembrane protein
 F;146-169/Domain: transmembrane #status predicted <TM1>
 F;177-196/Domain: transmembrane #status predicted <TM2>
 F;228-246/Domain: transmembrane #status predicted <TM3>
 F;268-287/Domain: transmembrane #status predicted <TM4>
 F;304-325/Domain: transmembrane #status predicted <TM5>
 F;352-371/Domain: transmembrane #status predicted <TM6>
 F;388-407/Domain: transmembrane #status predicted <TM7>
 F;63,82,115/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 Db 172 LHCTRNYYH 180

RESULT 23
 A46172
 Glucagon-like peptide 1 receptor - rat
 N;Alternate names: GLP-1 receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 24-Sep-1999
 C;Accession: A46172; I53420; I59231
 R;Thorens, B.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8641-8645, 1992
 A;Title: Expression cloning of the pancreatic beta cell receptor for the gluco-incretin
 A;Reference number: A46172; MUID:92409572; PMID:1326760
 A;Accession: A46172
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-463 <THO>
 A;Cross-references: GB:M97797; NID:g204326; PIDN:AAA73377.1; PID:g387868
 A;Experimental source: pancreatic islet cells
 A;Note: sequence extracted from NCBI backbone
 R;Lankat-Buttgeit, B.; Goke, R.; Fehmann, H.C.; Richter, G.; Goke, B.
 Exp. Clin. Endocrinol. 102, 341-347, 1994
 A;Title: Molecular cloning of a cDNA encoding for the GLP-1 receptor expressed in rat l
 A;Reference number: I53420; MUID:95112989; PMID:7813606
 A;Accession: I53420
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-322, 'I', 324-463 <RES>

A;Cross-references: GB:S75952; NID:g913834
 C;Superfamily: glucagon receptor
 C;Keywords: transmembrane protein

Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 Db 172 LHCTRNYYH 180

RESULT 24
 I84494
 glucagon-like peptide-1 receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Sep-1999
 C;Accession: I84494
 R;Thorens, B.; Porret, A.; Buehler, L.; Deng, S.; Morel, P.; Widmann, C.
 Diabetes 42, 1678-1682, 1993
 A;Title: Cloning and functional expression of the human islet GLP-1 receptor. Demonst
 A;Reference number: I38653; MUID:94009966; PMID:8405712
 A;Accession: I84494
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-463 <RES>
 A;Cross-references: EMBL:U01104; NID:g405081; PIDN:AAA03614.1; PID:g405082
 C;Genetics:
 A;Gene: GDB:GLP1R
 A;Cross-references: GDB:I37218; OMIM:I38032
 A;Map position: 6p21-6p21
 C;Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 Db 172 LHCTRNYYH 180

RESULT 25
 JN0616
 pituitary adenylate cyclase-activating polypeptide receptor 46-5 precursor - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 08-Oct-1999
 C;Accession: JN0616; S36768
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; P
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the recept
 A;Reference number: JN0616; MUID:93326107; PMID:7687425
 A;Accession: JN0616
 A;Molecule type: mRNA
 A;Residues: 1-467 <HOS>
 A;Experimental source: brain
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.;
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP recept
 A;Reference number: S36768; MUID:93326505; PMID:8396727
 A;Accession: S36768
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-467 <SPE>
 A;Cross-references: EMBL:Z33279; NID:g404252; PIDN:CAA80817.1; PID:g404253
 C;Superfamily: glucagon receptor
 C;Keywords: alternative splicing; glycoprotein; receptor
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-467/Product: pituitary adenylate cyclase-activating polypeptide receptor 46-5 #s
 F;47,59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSMFLRA 191
 Db 191 LFVSMFLRA 199
 |||||

RESULT 26
 JQ1957
 glucagon receptor - rat
 C;Alternate names: GLP-1 receptor homolog, hepatic
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
 C;Accession: JQ1957; A46211; S29689
 R;Svoboda, M.; Ciccarelli, B.; Tastenoy, M.; Cauvin, A.; Stievenart, M.; Charistophe, J.
 Biochem. Biophys. Res. Commun. 191, 479-486, 1993
 A;Title: Small introns in a hepatic cDNA encoding a new glucagon-like peptide 1-type rec
 A;Reference number: JQ1957; MUID:93213282; PMID:8384842
 A;Accession: JQ1957
 A;Molecule type: mRNA
 A;Residues: 1-485 <SVO>
 A;Cross-references: GB:X68692
 A;Experimental source: liver
 R;Delinek, L.J.; Lok, S.; Rosenberg, G.B.; Smith, R.A.; Grant, F.J.; Biggs, S.; Bensch,
 rnan, P.A.; Kindavogel, W.
 Science 259, 1614-1616, 1993
 A;Title: Expression cloning and signaling properties of the rat glucagon receptor.
 A;Reference number: A46211; MUID:93206096; PMID:8384375
 A;Accession: A46211
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A;Molecule type: mRNA
 A;Residues: 1-37,'W',217-323,'V',325-485 <JEL>
 A;Experimental source: liver
 A;Note: sequence extracted from NCBI backbone (NCBIP:127785)
 C;Genetics:
 A;Introns: 132/3; 168/2; 220/3; 407/3
 C;Superfamily: glucagon receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; liver; phosphoprotein; transmembra
 F;144-167/Domain: transmembrane #status predicted <TM1>
 F;175-194/Domain: transmembrane #status predicted <TM2>
 F;227-251/Domain: transmembrane #status predicted <TM3>
 F;264-286/Domain: transmembrane #status predicted <TM4>
 F;305-324/Domain: transmembrane #status predicted <TM5>
 F;352-370/Domain: transmembrane #status predicted <TM6>
 F;389-405/Domain: transmembrane #status predicted <TM7>
 F;47,60,75,79/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;432/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 Db 170 LHCTRNYYH 178
 |||||

RESULT 27
 JQ4363
 glucagon receptor precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 21-Jul-2000
 C;Accession: JQ4363
 R;Burrellin, R.; Li, J.; Charron, M.J.
 Gene 164, 305-310, 1995
 A;Title: Cloning and sequence analysis of the murine glucagon receptor-encoding gene.
 A;Reference number: JQ4363; MUID:96069600; PMID:7590348
 A;Accession: JQ4363
 A;Molecule type: mRNA
 A;Residues: 1-485 <BUR>
 A;Cross-references: GB:L38612; NID:97274387; PIDN:AAF44749.1; PID:97274388

C;Comment: This receptor is a plasma membrane glycoprotein that belongs to a subfamily
 genolysis and gluconeogenesis in li ver and insulin secretion by beta cells.
 C;Genetics:
 A;Gene: gr
 A;Introns: 21/3; 55/1; 91/1; 132/3; 168/2; 220/3; 273/1; 294/2; 317/3; 347/2; 393/3;
 C;Superfamily: glucagon receptor
 C;Keywords: glycoprotein; receptor; transmembrane protein
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-485/Product: glucagon receptor #status predicted <MAT>
 F;145-168/Domain: transmembrane #status predicted <TM1>
 F;176-196/Domain: transmembrane #status predicted <TM2>
 F;225-239/Domain: transmembrane #status predicted <TM3>
 F;247-258/Domain: transmembrane #status predicted <TM4>
 F;266-288/Domain: transmembrane #status predicted <TM5>
 F;304-331/Domain: transmembrane #status predicted <TM6>
 F;354-369/Domain: transmembrane #status predicted <TM7>
 F;386-405/Domain: transmembrane #status predicted <TM8>
 F;47,60,65,75,79,118/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYYH 180
 Db 170 LHCTRNYYH 178
 |||||

RESULT 28
 S36114
 pituitary adenylyate cyclase-activating polypeptide type I receptor precursor - rat
 A;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
 C;Accession: S36114; JN0617; S39062; S39063; PNO609; I58147; A48204
 R;Morrow, J.A.; Lutz, E.M.; West, K.M.; Fink, G.; Harmar, A.J.
 FEBS Lett. 329, 99-105, 1993
 A;Title: Molecular cloning and expression of a cDNA encoding a receptor for pituitary
 A;Reference number: S36114; MUID:93359075; PMID:8394834
 A;Accession: S36114
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-495 <MOR>
 A;Cross-references: EMBL:Z23282; NID:9397520; PIDN:CAA80820.1; PID:9397521
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.;
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the recep
 A;Reference number: JN0616; MUID:93326107; PMID:7687425
 A;Accession: JN0617
 A;Molecule type: mRNA
 A;Residues: 1-495 <HOS>
 A;Experimental source: brain
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP recep
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S39062
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-495 <SPR>
 A;Cross-references: EMBL:Z23274; NID:9404220; PIDN:CAA80812.1; PID:9404221
 A;Accession: S39063
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-348,350-495 <SP2>
 A;Cross-references: EMBL:Z23275; NID:9404197; PIDN:CAA80813.1; PID:9404198
 R;Svoboda, M.; Tastenoy, M.; Ciccarelli, B.; Stievenart, M.; Christophe, J.
 Biochem. Biophys. Res. Commun. 195, 881-888, 1993
 A;Title: Cloning of a splice variant of the pituitary adenylyate cyclase-activating p
 A;Reference number: PNO608; MUID:93384616; PMID:8396930
 A;Accession: PNO608
 A;Molecule type: mRNA
 A;Residues: 78-495 <SVO>

A;Accession: PM0609
 A;Molecule type: protein
 A;Residues: 349-376 <SV2>
 R;Hashimoto, H.; Ishihara, T.; Shigemoto, R.; Mori, K.; Nagata, S.
 Neuron 11, 333-342, 1993
 A;Title: Molecular cloning and tissue distribution of a receptor for pituitary adenylate
 A;Reference number: 158147; MUID:93357025; PMID:8394723
 A;Accession: I58147
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-495 <RES>
 A;Cross-references: GB:D16465; NID:g404381; PIDN:BAA03932.1; PID:g457661
 R;Pisegna, J.R.; Wank, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6345-6349, 1993
 A;Title: Molecular cloning and functional expression of the pituitary adenylate cyclase-
 A;Reference number: A48204; MUID:93317678; PMID:8392197
 A;Accession: A48204
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-420, 'L', 422-495 <PIS>
 A;Cross-references: GB:L16680; NID:g347941; PIDN:AAA41792.1; PID:g347942
 A;Comment: This protein stimulates both adenylate cyclase and phospholipase C and dually
 C;Superfamily: glucagon receptor
 C;Keywords: alternative splicing; anterior pituitary; G protein-coupled receptor; glycoprotein; pituitary adenylate cyclase-activating polypeptide receptor long form #
 F;1-347/376-495/Product: pituitary adenylate cyclase-activating polypeptide receptor short form #
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-495/Product: pituitary adenylate cyclase-activating polypeptide type I receptor #st
 F;155-177/Domain: transmembrane #status predicted <TM1>
 F;186-204/Domain: transmembrane #status predicted <TM2>
 F;227-252/Domain: transmembrane #status predicted <TM3>
 F;268-290/Domain: transmembrane #status predicted <TM4>
 F;308-331/Domain: transmembrane #status predicted <TM5>
 F;378-398/Domain: transmembrane #status predicted <TM6>
 F;413-433/Domain: transmembrane #status predicted <TM7>
 F;475/59,116,299,342,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;365,444/Binding site: phosphate (Ser) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LFVSPMLRA 191
 Db 191 LFVSPMLRA 199

RESULT 29
 S39061
 pituitary adenylate cyclase activating-peptide receptor form 3 - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
 C;Accession: S39061
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor.
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S39061
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-495 <SPE>
 A;Cross-references: EMBL:Z23273; NID:g404210; PIDN:CAA80811.1; PID:g404211
 C;Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LFVSPMLRA 191
 Db 191 LFVSPMLRA 199

RESULT 30
 S47631
 pituitary adenylate cyclase-activating polypeptide type I receptor precursor - bovine
 N;Alternate names: PACAP receptor
 C;Accession: S47631
 R;Miyamoto, Y.; Habata, Y.; Ohtaki, T.; Masuda, Y.; Ogi, K.; Onda, H.; Fujino, M.
 Biochim. Biophys. Acta 1218, 297-307, 1994
 A;Title: Cloning and expression of a complementary DNA encoding the bovine receptor f
 A;Reference number: S47631; MUID:94325336; PMID:8049255
 A;Accession: S47631
 A;Molecule type: mRNA
 A;Residues: 1-513 <MIY>
 A;Cross-references: EMBL:D17290; NID:g602765; PIDN:BAA04122.1; PID:g1374682
 A;Experimental source: brain
 A;Accession: S47632
 A;Molecule type: protein
 A;Residues: 38-41, 'X', 43-50, 'X', 52-66 <MI2>
 A;Experimental source: brain
 C;Genetics: 366/2
 C;Function:
 C;Superfamily: stimulates both adenylate cyclase and phospholipase C
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; phosphop
 F;1-37/Domain: signal sequence #status predicted <SIG>
 F;38-513/Product: pituitary adenylate cyclase-activating polypeptide type I receptor
 F;38-365,394-513/Product: pituitary adenylate cyclase-activating polypeptide type I r
 F;173-195/Domain: transmembrane #status predicted <TM1>
 F;204-222/Domain: transmembrane #status predicted <TM2>
 F;245-270/Domain: transmembrane #status predicted <TM3>
 F;286-308/Domain: transmembrane #status predicted <TM4>
 F;326-349/Domain: transmembrane #status predicted <TM5>
 F;396-416/Domain: transmembrane #status predicted <TM6>
 F;431-451/Domain: transmembrane #status predicted <TM7>
 F;65,77,134,360,420/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;383,462/Binding site: phosphate (Ser) (covalent) #status predicted
 Query Match 1.7%; Score 9; DB 2; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LFVSPMLRA 191
 Db 209 LFVSPMLRA 217

RESULT 31
 S39060
 pituitary adenylate cyclase activating-peptide receptor form 2 - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C;Accession: S39060
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP recept
 A;Reference number: S36768; MUID:93382505; PMID:8396727
 A;Accession: S39060
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-523 <SPE>
 A;Cross-references: EMBL:Z23272; NID:g404195; PIDN:CAA80810.1; PID:g404196
 C;Superfamily: glucagon receptor

Query Match 1.7%; Score 9; DB 2; Length 523;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LFVSPMLRA 191

Db 191 LFVSEMLRA 199
|||||

RESULT 32

JN0902

pituitary adenylate cyclase activating peptide receptor type I precursor - human

C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
C:Accession: JN0902
R:Ogi, K.; Miyamoto, Y.; Masuda, Y.; Habata, Y.; Hosoya, M.; Ohtaki, T.; Masuo, Y.; Onda
Biochem. Biophys. Res. Commun. 196, 1511-1521, 1993
A:Title: Molecular cloning and functional expression of a cDNA encoding a human pituitary
A:Reference number: JN0902; MUID:94071918; PMID:7902709
A:Accession: JN0902

A:Molecule type: mRNA

A:Residues: 1-525 <OGI>

A:Cross-references: DDBJ:U17516; NID:9457562; PIDN:BAA04466.1; PID:9540518

A:Experimental source: pituitary

C:Comment: This protein plays pivotal roles as a neurotransmitter and a neuromodulator,

C:Superfamily: glucagon receptor

C:Keywords: glycoprotein; neurotransmitter; receptor

F:1-77/Domain: signal sequence #status predicted <SIG>

F:78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #status
F:105,117,174,357,400,432/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 1.7%; Score 9; DB 2; Length 525;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSEMLRA 191

Db 249 LFVSEMLRA 257

RESULT 33

I38879

corticotropin releasing hormone receptor variant - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38879

R:Ross, P.C.; Kostas, C.M.; Ramabhadran, T.V.

Biochem. Biophys. Res. Commun. 205, 1836-1842, 1994

A:Title: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning,

A:Reference number: I38879; MUID:95110332; PMID:7811272

A:Accession: I38879

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-375 <RES>

A:Cross-references: EMBL:U16273; NID:9606973; PIDN:AAC50073.1; PID:9606974

C:Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 375;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410

Db 313 SFQGFVVS 320

RESULT 34

A55610

corticotropin-releasing factor receptor subtype 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999

C:Accession: A55610

R:Lovenberg, T.W.; Liaw, C.W.; Grigoriadis, D.E.; Cleverger, W.; Chalmers, D.T.; De Souza

Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995

A:Title: Cloning and characterization of a functionally distinct corticotropin-releasing

A:Reference number: A55610; MUID:95148632; PMID:7846062

A:Accession: A55610

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA
A:Residues: 1-411 <LOV>
A:Cross-references: EMBL:U16253; NID:9644771; PIDN:AAC52159.1; PID:9644772
C:Genetics:
A:Gene: CRF2R
C:Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410

Db 349 SFQGFVVS 356

RESULT 35

S26195

probable carboxyl-terminal processing proteinase - *Synechococcus* sp. (PCC 7002) (frag
C:Species: *Synechococcus* sp.
A:Variety: PCC 7002

C:Date: 07-May-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
C:Accession: S26195; S18125
R:Brand, S.N.; Tan, X.; Widger, W.R.

Plant Mol. Biol. 20, 481-491, 1992

A:Title: Cloning and sequencing of the petBD operon from the cyanobacterium *Synechococ*
A:Reference number: S26193; MUID:93043038; PMID:1421151

A:Accession: S26195

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-411 <BRA>

A:Cross-references: EMBL:X63049; NID:938962; PIDN:CAA44776.1; PID:938965

C:Superfamily: carboxyl-terminal processing proteinase

Query Match 1.5%; Score 8; DB 2; Length 411;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 LVLVLVFG 373

Db 15 LVLVLVFG 22

RESULT 36

S39535

corticotropin-releasing hormone receptor - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C:Accession: S39535

R:Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.

FEBS Lett. 335, 1-5, 1993

A:Title: Primary structure and functional expression of mouse pituitary and human br
A:Reference number: S39534; MUID:94063063; PMID:8243652

A:Accession: S39535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-415 <VIT>

A:Cross-references: EMBL:X72305; NID:9436120; PIDN:CAA51053.1; PID:9436121

A:Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an

C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 1.5%; Score 8; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410

Db 353 SFQGFVVS 360

RESULT 37

I58144

corticotropin-releasing factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: I58144
R;Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1195, 1993
A;Title: Identification of a seven transmembrane helix receptor for corticotropin-releasing factor
A;Reference number: I58144; MUID:94099969; PMID:8274282
A;Accession: I58144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-415 <RES>
A;Cross-references: GB:I25438; NID:9450298; PIDN:AAAL6441.1; PID:9457615
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||
DB 353 SFQGFVVS 360

RESULT 38

A56726
corticoliberin receptor precursor, cardiac - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 24-Nov-1999
C;Accession: A56726
R;Stenzel, P.; Keasterson, R.; Yeung, W.; Cone, R.D.; Rittenberg, M.B.; Stenzel-Poore, M.
Mol. Endocrinol. 9, 637-645, 1995
A;Title: Identification of a novel murine receptor for corticotropin-releasing hormone
A;Reference number: A56726; MUID:96015396; PMID:7565810
A;Accession: A56726
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-430 <STE>
A;Cross-references: GB:U19939; NID:9806763; PIDN:AA52243.1; PID:9806764
C;Superfamily: glucagon receptor
C;Keywords: cardiac muscle; heart

Query Match 1.5%; Score 8; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||
DB 368 SFQGFVVS 375

RESULT 39

I49279
sauvagine/corticotropin-releasing factor receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49279
R;Kishimoto, T.; Pearce, R.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 1108-1112, 1995
A;Title: A sauvagine/corticotropin-releasing factor receptor expressed in heart and skeletal muscle
A;Reference number: I49279; MUID:95166778; PMID:7755719
A;Accession: I49279
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-431 <KIS>
A;Cross-references: EMBL:U21729; NID:9717137; PIDN:AA52174.1; PID:9717138
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410

DB 369 SFQGFVVS 376
|||||

RESULT 40

CRF receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Accession: I49149
R;Perrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren, T.; Bilezikian, L.; Saw
Proc. Natl. Acad. Sci. U.S.A. 92, 2969-2973, 1995
A;Title: Identification of a second corticotropin-releasing factor receptor gene and
A;Reference number: I49149; MUID:95224061; PMID:7708757
A;Accession: I49149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-431 <RES>
A;Cross-references: EMBL:U17858; NID:9727254; PIDN:AAA68026.1; PID:9727255
C;Superfamily: glucagon receptor

Query Match 1.5%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
|||||

DB 369 SFQGFVVS 376
|||||

RESULT 41

A48260
corticoliberin receptor, long splice form - human
N;Alternate names: corticoliberin binding protein; corticotropin releasing factor rec
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 11-Apr-1997 #text_change 21-Jul-2000
C;Accession: I60975; A48260; S39534
R;Chen, R.; Lewis, K.A.; Perrin, M.H.; Vale, W.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 8967-8971, 1993
A;Title: Expression cloning of a human corticotropin-releasing factor (CRF) receptor.
A;Reference number: A48260; MUID:94022296; PMID:7692441
A;Accession: I60975
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-444 <RES>
A;Cross-references: GB:I23333; NID:9408691; PIDN:AAA35719.1; PID:9408692
A;Experimental source: Cushing corticotropic cell tumor
A;Accession: A48260
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <RE2>
A;Cross-references: GB:I23332; NID:9408689; PIDN:AAA35718.1; PID:9408690
R;Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.
FEBS Lett. 335, 1-5, 1993
A;Title: Primary structure and functional expression of mouse pituitary and human bra
A;Reference number: S39534; MUID:94063063; PMID:8243652
A;Accession: S39534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145,175-444 <VIT>
A;Cross-references: EMBL:X72304; NID:9436118; PIDN:CRA51052.1; PID:9436119
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 3 in having an a
C;Genetics:
A;Gene: GDB:CRHR1; CRHR; CRF-R; CRF1
A;Cross-references: GDB:235922; OMIM:122561
A;Map position: 17q12-17q22
C;Superfamily: glucagon receptor
C;Keywords: alternative splicing; transmembrane protein

Query Match 1.5%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
 DB 382 SFQGFVS 389

RESULT 42

GRBYCP

cytosine/purine transport protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: cytosine/purine permease; protein YER056C

C;Species: Saccharomyces cerevisiae

C;Date: 31-Dec-1992 #sequence_revision 19-May-1995 #text_change 05-Nov-1999

C;Accession: S50559; S20153

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612.

A;Reference number: S50559

A;Accession: S50559

A;Molecule type: DNA

A;Residues: 1-533 <DIE>

A;Cross-references: EMBL:U18813; NID:G1381127; PIDN:AAB64592.1; PID:G603292; GSPDB:GN000

A;Experimental source: strain S288c (AB972)

R;Weber, E.; Rodriguez, C.; Chevallier, M.R.; Jund, R.

Mol. Microbiol. 4, 585-596, 1990

A;Title: The purine-cytosine permease Gene of Saccharomyces cerevisiae: primary structure

A;Reference number: S20153; MUID:90279501; PMID:2191181

A;Accession: S20153

A;Molecule type: DNA

A;Residues: 1-191, 'M', 193-260, 'G', 262-533 <WEB>

A;Cross-references: EMBL:X51751; NID:G3699; PIDN:CAA36040.1; PID:G3700

A;Experimental source: strain FL100

C;Genetics:

A;Gene: SGD:FCY2; MIPS:YER056C

A;Cross-references: SGD:S0000858; MIPS:YER056C

A;Map position: 5R

C;Superfamily: cytosine/purine transport protein

C;Keywords: Glycoprotein; transmembrane protein

F;99-119/Domain: transmembrane #status predicted <TM1>

F;122-142/Domain: transmembrane #status predicted <TM2>

F;143-198/Domain: extracellular #status predicted <EXT>

F;199-221/Domain: transmembrane #status predicted <TM3>

F;257-277/Domain: transmembrane #status predicted <TM4>

F;301-320/Domain: transmembrane #status predicted <TM5>

F;345-368/Domain: transmembrane #status predicted <TM6>

F;398-419/Domain: transmembrane #status predicted <TM7>

F;466-485/Domain: transmembrane #status predicted <TM8>

F;160,181/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.5% Score 8; DB 1; Length 533;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 LIFVAFVS 271
 DB 133 LIFVAFVS 140

RESULT 43

T13256

tail-host specificity protein homolog - Lactococcus lactis phage BK5-T

C;Species: Lactococcus lactis phage BK5-T

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C;Accession: T13256

R;Boyce, J.D.; Davidson, B.E.; Hillier, A.J.

Appl. Environ. Microbiol. 61, 4089-4098, 1995

A;Title: Sequence analysis of the temperate Lactococcus lactis bacteriophage BK5-T and d

A;Reference number: 217646; MUID:96064422; PMID:8526523

A;Accession: T13256

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1904 <BOY>

A;Cross-references: EMBL:L44593; NID:G928826; PID:G928826; PIDN:AAA98579.1

Query Match

1.5%; Score 8; DB 2; Length 1904;

Best Local Similarity 100.0%; Pred. No. 43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
 DB 1773 SFQGFVS 1780

RESULT 44

B37334

L-mandelate dehydrogenase (EC 1.1.2.-) - Acinetobacter calcoaceticus (fragment)

C;Species: Acinetobacter calcoaceticus

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 13-Sep-1998

C;Accession: B37334

R;Fewson, C.A.

submitted to the Protein Sequence Database, October 1992

A;Reference number: A37334

A;Accession: B37334

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-50 <FEW>

C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology

C;Keywords: oxidoreductase

Query Match 1.3%; Score 7; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 KLAESTL 366
 DB 12 KLAESTL 18

RESULT 45

AB2755

host factor I [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C;Accession: AB2755

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woc

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; MCCI

r, Karp, P.; Romero, E.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB2755

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <KUR>

A;Cross-references: GB:AF008688; PIDN:AAL42456.1; PID:G17739871; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: hfg

A;Map position: circular chromosome

C;Superfamily: host factor I

Query Match 1.3%; Score 7; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 LFLNTVR 338
 DB 11 LFLNTVR 17

RESULT 46

C83574

hypothetical protein PA0570 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: C83574

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: AB2950; MUID:20437337; PMID:10984043
 A;Accession: C83574
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-115 <STO>
 A;Cross-references: GB:AE004493; GB:AE004091; NID:g9946436; PIDN:AG03959.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA0570

Query Match 1.3%; Score 7; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 PAAFWAA 293
 Db 17 PAAFWAA 23
 |||||

RESULT 47
 C72654
 Hypothetical protein APE0663 - *Aeropyrum pernix* (strain K1)
 C;Species: *Aeropyrum pernix*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
 C;Accession: C72654
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kana, H.
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum pernix*
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: C72654
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-116 <RAW>
 A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79635.1; PID:d1043421; PID:g5104188
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0663
 C;Superfamily: *Aeropyrum pernix* hypothetical protein APE0663

Query Match 1.3%; Score 7; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 ILVEGLY 260
 Db 45 ILVEGLY 51
 |||||

RESULT 48
 H70787
 Hypothetical protein Rv3655c - *Mycobacterium tuberculosis* (strain H37Rv)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: H70787
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: H70787
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-125 <COL>
 A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA17977.1; PID:g296007
 A;Experimental source: strain H37Rv

C;Genetics:
 A;Gene: Rv3655c
 C;Superfamily: *Mycobacterium tuberculosis* hypothetical protein Rv3655c

Query Match 1.3%; Score 7; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 TLVLVLV 371
 Db 9 TLVLVLV 15
 |||||

RESULT 49

ZBBPT4

gene 57B protein - phage T4

C;Species: phage T4

A;Note: host *Escherichia coli*

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 23-Jul-1999

C;Accession: A04311

R;Broids, J.; Abelson, J.

J. Mol. Biol. 185, 545-563, 1985

A;Title: Sequence organization and control of transcription in the bacteriophage T4

A;Reference number: A92919; MUID:86037230; PMID:4057254

A;Accession: A04311

A;Molecule type: DNA

A;Residues: 1-152 <BRO>

A;Cross-references: GB:X03016; GB:J02511; GB:J02516; GB:J02517; GB:V00861; GB:V00862;

C;Genetics:

A;Gene: 57B

C;Superfamily: phage T4 gene 57B protein

Query Match

1.3%; Score 7; DB 1; Length 152;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 STLVLVL 370

Db 80 STLVLVL 86

|||||

RESULT 50

B85360

hypothetical protein A7930770 [imported] - *Arabidopsis thaliana*C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C;Accession: B85360

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory

A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85360

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-157 <STO>

A;Cross-references: GB:NC_001268; NID:g7269978; PIDN:CAB79795.1; GSPDB:GN00140

C;Genetics:

A;Gene: A7930770

A;Map position: 4

Query Match

1.3%; Score 7; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 IVFVCLP 383

Db 49 IVFVCLP 55

|||||

Search completed: December 9, 2003, 09:02:39

Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:45:50, Search time 17 seconds
(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLVWGLMGLSCL.....DDILMEKPSRPMESNPDTG 541

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	363	67.1	550	1 PTH2_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTH2_RAT	P70555 rattus norv
3	25	4.6	585	1 PTH2_DIDMA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTH2_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTH2_MOUSE	P41593 mus musculu
8	18	3.3	591	1 PTH2_RAT	P25961 rattus norv
9	18	3.3	593	1 PTH2_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	O46502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 VIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	457	1 VIPR_MELGA	Q31085 meleagris g
15	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
16	13	2.4	459	1 VIPR_MOUSE	P97751 mus musculu
17	13	2.4	459	1 VIPR_RAT	P30083 rattus norv
18	13	2.4	462	1 GIPR_MESAU	P43218 mesocricetu
19	12	2.2	466	1 GIPR_HUMAN	P48546 homo sapien
20	10	1.8	477	1 GIPR_HUMAN	P47871 homo sapien
21	10	1.8	550	1 GLP2_RAT	Q92040 rattus norv
22	10	1.8	553	1 GLP2_HUMAN	O95838 homo sapien
23	9	1.7	437	1 VIPR_MOUSE	P41588 mus musculu
24	9	1.7	437	1 VIPR_RAT	P35000 rattus norv
25	9	1.7	438	1 VIPR_HUMAN	P41587 homo sapien
26	9	1.7	463	1 GLP1_HUMAN	P43220 homo sapien
27	9	1.7	463	1 GLP1_RAT	P32301 rattus norv
28	9	1.7	468	1 PACR_HUMAN	P41586 homo sapien
29	9	1.7	485	1 GLR_MOUSE	Q61606 mus musculu
30	9	1.7	485	1 GLR_RAT	P30082 rattus norv
31	9	1.7	489	1 GLP1_MOUSE	O35659 mus musculu
32	9	1.7	496	1 GLP1_MOUSE	P70205 mus musculu
33	9	1.7	513	1 PACR_BOVIN	Q29627 bos taurus

RESULT 1

ID	PTH2_HUMAN	STANDARD	PRT	550 AA
AC	P49130;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Parathyroid hormone receptor precursor (PTH2 receptor).			
GN	PTH2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=95318121; PubMed=7797535;			
RA	Usdin T.B., Gruber C., Bonner T.I.;			
RT	"Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";			
RL	J. Biol. Chem. 270:15455-15458(1995).			
RN	[2]			
RP	SEQUENCE OF 26-40 AND 306-550 FROM N.A.			
RX	MEDLINE=9707671; PubMed=8921382;			
RA	Usdin T.B., Modi W., Bonner T.I.;			
RT	"Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33 by fluorescence in situ hybridization.";			
RL	Genomics 37:140-141(1996).			
CC	-1- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.			
CC	-1- ALSO EXPRESSED IN THE TESTIS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC				
DR	EMBL; U35128; AAC50157.1; -			
DR	EMBL; U47124; AAC96796.1; -			
DR	EMBL; U47129; AAC50767.1; -			
DR	EMBL; U47125; AAC50767.1; JOINED.			
DR	EMBL; U47126; AAC50767.1; JOINED.			
DR	EMBL; U47127; AAC50767.1; JOINED.			
DR	EMBL; U47128; AAC50767.1; JOINED.			
DR	PIR; A57519; A57519.			
DR	Genew; HGNC:9609; PTHR2.			
DR	MIM; 601469; -			
DR	GO; GO:0005887; C-integral to plasma membrane; TAS			
DR	GO; GO:0004991; P-parathyroid hormone receptor activity; TAS.			
DR	GO; GO:0007186; P-g-protein coupled receptor protein signalin. . .; TAS.			

P32215 rattus norv
P28217 styela plic
Q13324 homo sapien
P47866 rattus norv
P42784 synechococc
O42603 xenopus lae
P35347 mus musculu
P35353 rattus norv
O62772 ovine aries
Q46002 xenopus lae
Q90812 gallus gall
Q60748 mus musculu

```

DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormu_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Horm; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 550
FT PARATHYROID HORMONE RECEPTOR.
FT DOMAIN 27 145
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 167
FT DOMAIN 170 176
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 196
FT DOMAIN 197 237
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260
FT DOMAIN 261 275
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 297
FT DOMAIN 298 316
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 317 337
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 338 364
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 365 383
FT DOMAIN 384 394
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 395 417
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 418 550
FT CARBOHYD 51
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 62235 MW; 2ADD14DBA68A9BF8 CRC64;

Query Match 67.1%; Score 363; DB 1; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLVHGWMMLGSCLLARAQSDGTTTIEEQIVLVKAKVQCELNITAQLQEGNCG 63
DB 4 LGASLVHGWMMLGSCLLARAQSDGTTTIEEQIVLVKAKVQCELNITAQLQEGNCG 63
QY 64 FEWDGLICWPRTGTVGKI SAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTYWYS 123
DB 64 FEWDGLICWPRTGTVGKI SAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTYWYS 123
QY 124 DCLRFLOPDISIGKQBFCEFLVYVYVYSGISLAVAILLIGYFRRLHCTRYIHMH 183
DB 124 DCLRFLOPDISIGKQBFCEFLVYVYVYSGISLAVAILLIGYFRRLHCTRYIHMH 183
QY 184 FVSFMLRATSI FVKDVRVHAHIGVKLESLIMQDDPQNSIATSVDKSQYIGCKIAVNF 243
DB 184 FVSFMLRATSI FVKDVRVHAHIGVKLESLIMQDDPQNSIATSVDKSQYIGCKIAVNF 243
QY 244 IYFLATNYWILVEGLYLNHLIFVAFPSDKYLVGLFWGFPFAFVAAMAVARATLAD 303
DB 244 IYFLATNYWILVEGLYLNHLIFVAFPSDKYLVGLFWGFPFAFVAAMAVARATLAD 303
QY 304 ARCWELSGADIKWYQAPILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYKRLAK 363
DB 304 ARCWELSGADIKWYQAPILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYKRLAK 363
QY 364 STLVLVLFVGHVYVFCVLPHPSTGLGWEIRHMCFLFPNSFGFFVSIYICVNGEVOAE 423
DB 364 STLVLVLFVGHVYVFCVLPHPSTGLGWEIRHMCFLFPNSFGFFVSIYICVNGEVOAE 423
QY 424 VKKQWSRWNLVDWKTTPPCGSRRCGSLVLTVTWHTSSQSOVAA 467
DB 424 VKKQWSRWNLVDWKTTPPCGSRRCGSLVLTVTWHTSSQSOVAA 467

RESULT 2
PTH2_RAT

```

```

ID PTH2_RAT STANDARD; PRT; 546 AA.
AC P70555;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB Parathyroid hormone receptor precursor (PTH2 receptor).
GN PTHR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96426194; PubMed=8828488;
RA Usdin T.B., Bonner T.I., Hatt G., Mezey E.;
RT "Distribution of parathyroid hormone-2 receptor messenger ribonucleic
RT acid in rat.";
RL Endocrinology 137:4285-4297 (1996).
CC -|- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLYL CYCLASE. PTHR2 MAY BE RESPONSIBLE FOR PTH EFFECTS IN A
CC NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN
CC PANCREATIC FUNCTION. PTHR2 PRESENCE IN NEURONS INDICATES THAT IT
CC MAY FUNCTION AS A NEUROTRANSMITTER RECEPTOR.
CC -|- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN, ARTERIAL AND
CC CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM, IN THE HEAD OF THE
CC EPIDIDYMIS. LOWER EXPRESSION IS FOUND IN VASCULAR SMOOTH MUSCLE,
CC EXOCRINE PANCREAS, TESTIS AND PLACENTA.
CC -|- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U55836; AAC52849.1; -.
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR001879; hormu_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Horm; 1.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; FALSE_NEG.
CC PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
CC PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 546
FT PARATHYROID HORMONE RECEPTOR.
FT DOMAIN 27 143
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167
FT DOMAIN 168 174
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194
FT DOMAIN 195 235
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 258
FT DOMAIN 259 273
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 295
FT DOMAIN 296 313
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 334
FT DOMAIN 335 361
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 362 380
FT DOMAIN 381 391
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 392 414
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 415 546
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

```

Query Match 6.1%; Score 33; DB 1; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGYSISFGLAVAILIIGYFRLHCTRYNH 180
 DB 146 YTVGYSISFGLAVAILIIGYFRLHCTRYNH 178

RESULT 3

PTRR DIDMA STANDARD; PRT; 585 AA.

AC P25107;
 DT 01-NOV-1992 (Rel. 22, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHrP receptor).
 GN PTHR1 OR PTHR.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=3267;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92054592; PubMed=1658941;
 RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-P., Schipani E.,
 RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
 RA Kronenberg H.M., Segre G.V.; for parathyroid hormone and parathyroid
 RT hormone-related peptide.";
 RL Science 254:1024-1026(1991).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M74445; AAA30979.1; -;
 DR PIR; A39286; A39286.
 DR HSP; Q03431; IBL1.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm.2; 1.
 DR Pfam; PF02793; HEM_1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
 DR PROSITE; PS00650; G PROTEIN RECP F2_2; 1.
 DR PROSITE; PS00651; G PROTEIN RECP F2_3; 1.
 DR PROSITE; PS00652; G PROTEIN RECP F2_4; 1.
 DR PROSITE; PS00653; G PROTEIN RECP F2_5; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 585
 FT PARATHYROID HORMONE/PARATHYROID HORMONE-
 FT RELATED PEPTIDE RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT TRANSMEM 315

DOMAIN 337 355
 TRANSMEM 356 376
 DOMAIN 377 403
 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 404 422
 DOMAIN 423 434
 TRANSMEM 435 457
 DOMAIN 458 585
 BY SIMILARITY.
 DISULFID 48 114
 DISULFID 105 145
 DISULFID 128 167
 CARBOHYD 148 148
 CARBOHYD 158 158
 CARBOHYD 163 163
 CARBOHYD 173 173
 SEQUENCE 585 AA; 65963 MM; 34900384CD6DF477 CRC64;
 Query Match 4.6%; Score 25; DB 1; Length 585;
 Best Local Similarity 100.0%; Pred. No. 2.8e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNHMLFVFSFMLRA 191
 DB 207 GYFRLHCTRYNHMLFVFSFMLRA 231

RESULT 4

SCRC HUMAN STANDARD; PRT; 440 AA.
 ID SCRC HUMAN STANDARD; PRT; 440 AA.
 AC P47872; Q12961; Q13213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE secretin receptor precursor (SCT-R).
 GN SCTR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95169147; PubMed=7864894;
 RA Jiang S., Ulrich C.D.;
 RT "Molecular cloning and functional expression of a human pancreatic
 RT secretin receptor.";
 RL Biochem. Biophys. Res. Commun. 207:883-890(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95336443; PubMed=7612008;
 RA Chow B.K.-C.;
 RT "Molecular cloning and functional characterization of a human
 RT secretin receptor.";
 RL Biochem. Biophys. Res. Commun. 212:204-211(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=95214632; PubMed=7700244;
 RA Patel D.R., Kong Y., Sreedharan S.P.;
 RT "Molecular cloning and expression of a human secretin receptor.";
 RL Mol. Pharmacol. 47:467-473(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S.,
 RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U20178; AAC50106.1; -;
 DR EMBL; U28281; AAA87556.1; -;
 DR EMBL; U13989; AAA64949.1; -;
 DR EMBL; AB065660; BAC05886.1; -;
 DR PIR; JC2532; JC2532.
 DR Genew; HGNC:10608; SCTR.
 DR MIM; 182098; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015055; F:secretin receptor activity; TAS.
 DR GO; GO:0007586; P:digestion; TAS.
 DR GO; GO:0007588; P:excretion; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF000002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HormR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_4; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 440 SECRETIN RECEPTOR.
 FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 240 3 (POTENTIAL).
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 276 4 (POTENTIAL).
 FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 317 5 (POTENTIAL).
 FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 362 6 (POTENTIAL).
 FT DOMAIN 363 392 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 393 440 7 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 124 124 G -> A (IN REF. 1).
 FT CONFLICT 210 210 A -> P (IN REF. 2).
 FT CONFLICT 308 308 I -> F (IN REF. 3).
 FT CONFLICT 333 333 E -> Q (IN REF. 3).
 FT CONFLICT 377 377 G -> A (IN REF. 1).
 FT SEQUENCE 440 AA; 50206 MW; E22CDD08E7C0ACC1 CRC64;
 Query Match 3.5%; Score 19; DB 1; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 169 FRLHCTRYNHMLFVSP 187
 |||||
 Db 167 FRLHCTRYNHMLFVSP 185
 RESULT 5
 SCRC_RAT
 ID -SCRC_RAT STANDARD; PRT; 449 AA.

AC P23811;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Secretin receptor precursor (SCT-R).
 GN SCTR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91266890; PubMed=1646711;
 RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
 RA Nagata S.;
 RT "Molecular cloning and expression of a cDNA encoding the secretin
 RT receptor.";
 RL EMBO J. 10.1635-1641(1991).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X59132; CAA41849.1; -;
 DR PIR; S16319; S16319.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF000002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HormR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 449 SECRETIN RECEPTOR.
 FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 240 3 (POTENTIAL).
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 276 4 (POTENTIAL).
 FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 317 5 (POTENTIAL).
 FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 362 6 (POTENTIAL).
 FT DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 370 392 7 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;
 Query Match 3.5%; Score 19; DB 1; Length 449;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRLLHCTRYHMLFVSF 187
Db 167 FRRLLHCTRYHMLFVSF 185

RESULT 6
ID PTHR_PIG STANDARD; PRT; 585 AA.
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHr receptor).
GN PTHR1 OR PTHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A., Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for porcine parathyroid hormone/parathyroid hormone-related peptide receptor."
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18315; AAC48619.1; --
DR HSP; Q03431; IBL1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM_1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G PROTEIN RECP F2 1; 1.
DR PROSITE; PS00650; G PROTEIN RECP F2 2; 1.
DR PROSITE; PS00227; G PROTEIN RECP F2 3; 1.
DR PROSITE; PS00261; G PROTEIN RECP F2 4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 26
FT CHAIN 27 585
FT PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR.
FT FT 184
FT DOMAIN 27 184
FT TRANSMEM 185 208
FT DOMAIN 209 215
FT TRANSMEM 216 235
FT DOMAIN 236 277
FT TRANSMEM 278 301
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT DOMAIN 424 435
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 184 208
FT TRANSMEM 209 215
FT DOMAIN 216 235
FT TRANSMEM 236 277
FT DOMAIN 278 301
FT TRANSMEM 302 315
FT DOMAIN 316 337
FT TRANSMEM 338 356
FT DOMAIN 357 377
FT TRANSMEM 378 404
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 235
FT TRANSMEM 236 277
FT DOMAIN 278 301
FT TRANSMEM 302 315
FT DOMAIN 316 337
FT TRANSMEM 338 356
FT DOMAIN 357 377
FT TRANSMEM 378 404
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 236 277
FT TRANSMEM 278 301
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 301
FT TRANSMEM 302 315
FT DOMAIN 316 337
FT TRANSMEM 338 356
FT DOMAIN 357 377
FT TRANSMEM 378 404
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 316 337
FT TRANSMEM 338 356
FT DOMAIN 357 377
FT TRANSMEM 378 404
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 357 377
FT TRANSMEM 378 404
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 405 423
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 424 435
FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 436 458
FT DOMAIN 459 585
FT CYTOPLASMIC (POTENTIAL).
FT BY SIMILARITY.
FT DISULFID 104 144
FT BY SIMILARITY.
FT DISULFID 127 166
FT BY SIMILARITY.
FT CARBOHYD 147 147
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 162 162
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;
Query Match 3.3%; Score 18; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 245 YFLATNYWLVLEGLYH 262
Db 285 YFLATNYWLVLEGLYH 302

RESULT 7
ID PTHR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor precursor (PTH/PTHr receptor).
GN PTHR1 OR PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/HEHA;
RX MEDLINE=95034305; PubMed=7524627;
RA Karpier M., van Dijk T.B., Hoesjmakers T., Cremers F., Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes."
RL Mech. Dev. 47:29-42(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X78936; CAA55536.1; --
DR EMBL; L34611; AAA40011.1; --
DR EMBL; L34608; AAA40011.1; JOINED.
DR EMBL; L34607; AAA40011.1; JOINED.
DR EMBL; L34609; AAA40011.1; JOINED.

DR EMBL; L34610; AAA40011.1; JOINED.
 DR PIR; I59297; I59297.
 DR PIR; S44203; S44203.
 DR HSSP; Q03431; 1BL1.
 DR MGD; MGI:97801; Pchl1.
 DR GO; GO:0030282; P:bone mineralization; IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 591
 FT DOMAIN 27 188
 FT TRANSMEM 189 212
 FT DOMAIN 213 219
 FT TRANSMEM 220 239
 FT DOMAIN 240 282
 FT TRANSMEM 283 306
 FT DOMAIN 307 320
 FT TRANSMEM 321 342
 FT DOMAIN 343 361
 FT TRANSMEM 362 382
 FT DOMAIN 383 409
 FT TRANSMEM 410 428
 FT DOMAIN 429 440
 FT TRANSMEM 441 463
 FT DOMAIN 464 591
 FT DISULFID 48 117
 FT DISULFID 108 148
 FT DISULFID 131 170
 FT CARBOHYD 151 151
 FT CARBOHYD 161 161
 FT CARBOHYD 166 166
 FT CARBOHYD 176 176
 FT CONFLICT 27 28
 FT CONFLICT 464 465
 FT CONFLICT 500 501
 FT CONFLICT 501 501
 FT SEQUENCE 591 AA; 66313 MW; F7876F8D388BDDFD CRC64;
 Query Match 3.3%; Score 18; DB 1; Length 591;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWILVEGLYH 262
 DB 290 YFLATNYWILVEGLYH 307
 ID PTHR RAT STANDARD; PRT; 591 AA.
 AC P25961;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHr receptor).
 GN PTHR1 OR PTHR
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=92212903; PubMed=1313566;
 RA Abou-Samra A.-B., Jueppner H., Porce T., Freeman M.W., Kong X.-F.,
 RA Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
 RA Kronenberg H.M., Segre G.V.;
 RT "Expression cloning of a common receptor for parathyroid hormone and
 RT parathyroid hormone-related peptide from rat osteoblast-like cells: a
 RT single receptor stimulates intracellular accumulation of both cAMP
 RT and inositol trisphosphates and increases intracellular free
 RT calcium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94292182; PubMed=8020952;
 RA Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,
 RA Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
 RT "Cloning of a parathyroid hormone/parathyroid hormone-related peptide
 RT receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:
 RT chromosomal assignment of the gene in the human, mouse, and rat
 RT genomes.";
 RL Genomics 20:20-26(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M77184; AAA41811.1; -;
 DR PIR; I54195; I54195.
 DR HSSP; Q03431; 1BL1.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 591
 FT DOMAIN 27 188
 FT TRANSMEM 189 212
 FT DOMAIN 213 219
 FT TRANSMEM 220 239
 FT DOMAIN 240 282
 FT TRANSMEM 283 306
 FT DOMAIN 307 320
 FT TRANSMEM 321 342
 FT DOMAIN 343 361
 FT TRANSMEM 362 382
 FT DOMAIN 383 409
 FT TRANSMEM 410 428
 FT DOMAIN 429 440
 FT TRANSMEM 441 463
 FT DOMAIN 464 591
 FT DISULFID 48 117
 FT DISULFID 108 148
 FT DISULFID 131 170

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 591;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYIH 262
 DB 290 YFLATNYWILVEGLYIH 307

RESULT 9

PTTR_HUMAN STANDARD; PRT; 593 AA.

AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHrP receptor).
 GN PTHRI OR PTHR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93238641; PubMed=8386612;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RL Endocrinology 132:2157-2165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93387403; PubMed=8397094;
 RA Schneider H., Peyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263723; PubMed=7745008;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidke J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Pseudohypoparathyroidism type Ib is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=20374568; PubMed=10913300;
 RA Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schaefer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 168-198.

CC MEDLINE=98409426; PubMed=9737850;
 RA Pellegrini M., Bisello A., Rosenblatt M., Choev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT MURK-JANSEN ARG-223.
 RX MEDLINE=95215874; PubMed=7701349;
 RA Schipani E., Kruse K., Juppner H.;
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=8703170;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Juppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL New Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP MUTAGENESIS OF ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745;
 RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
 RA Juppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
 CC KIDNEY, BONE AND LIVER.
 CC -1- DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF BLOMSTRAND TYPE OF
 CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
 CC -1- DISEASE: DEFECTS IN PTHRI ARE THE CAUSE OF MURK-JANSEN TYPE OF
 CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
 CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
 CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
 CC HORMONES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L04308; AAA3525.1; -;
 CC EMBL; X68596; CAA48589.1; -;
 CC EMBL; U22409; AAB60657.1; -;
 CC EMBL; U22401; AAB60657.1; JOINED.
 CC EMBL; U22402; AAB60657.1; JOINED.
 CC EMBL; U22403; AAB60657.1; JOINED.
 CC EMBL; U22404; AAB60657.1; JOINED.
 CC EMBL; U22405; AAB60657.1; JOINED.
 CC EMBL; U22406; AAB60657.1; JOINED.
 CC EMBL; U22407; AAB60657.1; JOINED.
 CC EMBL; U22408; AAB60657.1; JOINED.
 CC EMBL; U17418; AAA56774.1; -;
 CC EMBL; I38139; A49191.
 CC PDB; 1BL1; 30-MAR-99.
 CC PDB; 1ET2; 06-SEP-00.
 CC PDB; 1ET3; 06-SEP-00.
 CC Genew; HGNC:9608; PTHRI.


```
DR MTM; 168468; --
DR MIM; 156400; --
DR MIM; 215045; --
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Disease mutation; 3D-structure; Dwarfism.
FT SIGNAL 1 26
FT CHAIN 27 593
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 593
FT DISULFID 48 117
FT DISULFID 108 148
FT DISULFID 131 170
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT VARIANT 223 223
FT VARIANT 410 410
FT CONFLICT 471 471
FT CONFLICT 473 473
FT HELIX 169 176
FT HELIX 180 185
FT HELIX 188 196
SQ SEQUENCE 593 AA; 66360 MW; DA1400640A6C7F2B CRC64;
Query Match 3.3%; Score 18; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEGLYLH 262
Db 290 YFLATNYWILVEGLYLH 307
RESULT 10
SCRC_RABIT
ID SCRC_RABIT STANDARD; PRT; 445 AA.
AC O46502;
DT 15-JUL-1999 (Rel. 38, Created)
```

```
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DR Secretin receptor precursor (SCT-R).
GN SCTR.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCBI_TaxID:9986; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:98366112; PubMed:9700755;
RA Svoboda M., Tastenoy M., de Neef P., Delporte C., Maelbroeck M.,
RA Robberecht P.;
RT "Molecular cloning and in vitro properties of the recombinant rabbit
RT secretin receptor.";
RL Peptides 19:1055-1062(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF025411; AAC32767.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 445
FT DOMAIN 22 139
FT TRANSMEM 140 163
FT DOMAIN 164 170
FT TRANSMEM 171 190
FT DOMAIN 191 212
FT TRANSMEM 213 236
FT DOMAIN 237 250
FT TRANSMEM 251 272
FT DOMAIN 273 290
FT TRANSMEM 291 313
FT DOMAIN 314 339
FT TRANSMEM 340 358
FT DOMAIN 359 365
FT TRANSMEM 366 388
FT DOMAIN 389 445
FT CARBOHYD 68 68
FT CARBOHYD 96 96
FT CARBOHYD 102 102
FT CARBOHYD 124 124
SQ SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;
Query Match 3.0%; Score 16; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 FRRLHCTRYIHMLHF 184
Db 163 FRRLHCTRYIHMLHF 178
```


RESULT 11

ID	VIPR_CARAU	STANDARD;	PRT;	447 AA.
AC	Q90308;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Vasodilative intestinal polypeptide receptor (VIP-R) (VIP receptor).			
OS	Carassius auratus (Goldfish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Carassius.			
OX	NCBI_TaxID=7957;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97190233; PubMed=9038250;			
RA	Chow B.K.C., Yuen T.T.H., Chan K.W.;			
RT	"Molecular evolution of vertebrate VIP receptors and functional			
RT	characterization of a VIP receptor from goldfish Carassius auratus.";			
RL	Gen. Comp. Endocrinol. 105:176-185 (1997).			
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS			
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIC			
CC	CYCLASE.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U56391; AAB05459.1; --			
DR	InterPro; IPR000832; GPCR secretin.			
DR	InterPro; IPR001879; hormn_receptor.			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	Pfam; PF02793; HRM; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	SMART; SM00008; Hormr; 1.			
DR	PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.			
DR	PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.			
DR	PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.			
DR	PROSITE; PS0281; G_PROTEIN_RECP_F2_4; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 103			
FT	TRANSMEM 104 128			
FT	DOMAIN 129 135			
FT	TRANSMEM 136 135			
FT	DOMAIN 156 178			
FT	TRANSMEM 179 202			
FT	DOMAIN 203 216			
FT	TRANSMEM 217 238			
FT	DOMAIN 239 256			
FT	TRANSMEM 257 280			
FT	DOMAIN 281 305			
FT	TRANSMEM 306 325			
FT	DOMAIN 326 337			
FT	TRANSMEM 338 357			
FT	DOMAIN 358 447			
FT	DISULFID 177 247			
FT	CARBOHYD 17 17			
FT	CARBOHYD 22 22			
FT	CARBOHYD 64 64			
FT	CARBOHYD 91 91			
FT	CARBOHYD 169 169			
SEQ	SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;			

Query Match 3.0%; Score 16; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 339 359 6 (POTENTIAL).

FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 375 395 7 (POTENTIAL).

FT DOMAIN 396 455 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.5e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTNRVYHM 181

DB 159 FRLHCTNRVYHM 171

RESULT 13

ID VIPR_HUMAN STANDARD; PRT; 457 AA.

AC P32241; Q15871; DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)

DE (Pituitary adenylate cyclase activating polypeptide type II receptor)

DE (PACAP type II receptor) (PACAP-R-2).

GN VIPR1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Intestine;

RX MEDLINE=93290641; PubMed=8390245;

RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;

RT "Cloning and functional expression of a human neuroendocrine

RT vasoactive intestinal peptide receptor.";

RL Biochem. Biophys. Res. Commun. 193:546-553 (1993).

RN [2]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC TISSUE=Intestine;

RX MEDLINE=94235025; PubMed=8179610;

RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maquet J.J., Carrero I.,

RA Ogier-Denis E., Laburthe M.;

RT "Human intestinal VIP receptor: cloning and functional expression of

RT two cDNA encoding proteins with different N-terminal domains.";

RL Biochem. Biophys. Res. Commun. 200:769-776 (1994).

RN [3]

RP SEQUENCE FROM N.A.

RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,

RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.;

RT "Genome-wide discovery and analysis of human seven transmembrane helix

RT receptor genes.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 33-457 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=95001220; PubMed=7917790;

RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;

RT "Molecular cloning and functional characterization of a human liver

RT vasoactive intestinal peptide receptor.";

RL Cell. Signal. 6:321-333 (1994).

RN [5]

RP DISULFIDE BOND.

RX MEDLINE=99126981; PubMed=9928020;

RA Knudsen S.M., Tams J.W., Wulff B.-S., Fahrenkrug J.;

RT "Importance of conserved cysteines in the extracellular loops of

RT human PACAP/VIP1 receptor for ligand binding and stimulation of cAMP

RT production.";

Ann. N.Y. Acad. Sci. 865:259-265 (1998).

-!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Short; Synonyms=hIVR8;

CC IsoId=P32241-1; Sequences=Displayed;

CC Name=Long; Synonyms=hIVR5;

CC IsoId=P32241-2; Sequences=VSP 002010;

-!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS, RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY, LIVER AND PLACENTA.

-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U11087; AAB60362.1; -

DR EMBL; U11079; AAB60362.1; JOINED.

DR EMBL; U11080; AAB60362.1; JOINED.

DR EMBL; U11081; AAB60362.1; JOINED.

DR EMBL; U11083; AAB60362.1; JOINED.

DR EMBL; U11084; AAB60362.1; JOINED.

DR EMBL; U11085; AAB60362.1; JOINED.

DR EMBL; U11086; AAB60362.1; JOINED.

DR EMBL; L13288; AAA36805.1; -

DR EMBL; X77777; CAA54814.1; -

DR EMBL; X75299; CAA53046.1; -

DR EMBL; AB05669; BAC05895.1; -

DR EMBL; L20295; AAA36802.1; -

DR PIR; JC2194; JC2194.

DR Genew; HGNC:12694; VIPR1.

DR MIM; 192321; -

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0044999; F:vasoactive intestinal polypeptide receptor . . .; TAS.

DR GO; GO:0007586; P:digestion; TAS.

DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.

DR GO; GO:0006955; P:immune response; TAS.

DR GO; GO:0006936; P:muscle contraction; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

DR GO; GO:0007268; P:synaptic transmission; TAS.

DR InterPro; IPR000832; GPCR_secretin.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PS00249; GPCRSSECRETIN.

DR SMART; SM00008; Hormk; 1.

DR PROSITE; PS00649; G-PROTEIN RECP F2_1; 1.

DR PROSITE; PS00650; G-PROTEIN RECP F2_2; 1.

DR PROSITE; PS02271; G-PROTEIN RECP F2_3; 1.

DR PROSITE; PS02611; G-PROTEIN RECP F2_4; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Alternative splicing.

FT SIGNAL 1 30

FT CHAIN 31 457

FT POTENTIAL.

FT VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1.

FT EXTRACELLULAR (POTENTIAL).

FT 1 (POTENTIAL).

FT CYTOPLASMIC (POTENTIAL).

FT 2 (POTENTIAL).

FT EXTRACELLULAR (POTENTIAL).

FT 3 (POTENTIAL).

FT CYTOPLASMIC (POTENTIAL).

FT 4 (POTENTIAL).

FT EXTRACELLULAR (POTENTIAL).

FT 5 (POTENTIAL).

```

FT DOMAIN 317 341 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 342 361 6 (POTENTIAL).
FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 393 7 (POTENTIAL).
FT DOMAIN 394 457 CYTOPLASMIC (POTENTIAL).
FT DISULFID 215 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 290 MPPSPFLPARMLCVLAGALAWAGPAGGOAAR -> MPPPPP
FT VARSPLIC 1 32 GVARRRLELEAARSLLGSS (in isoform Long).
FT FTID-VSP_002010.
FT CONFLICT 284 284 G -> GLLR (IN REF. 2).
FT SEQUENCE 457 AA; 51547 MW; DAA40CF5BEC47D7D CRC64;

Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
Db |||||
170 LHCTRNVIHMLF 182

RESULT 14
ID VIPR MELGA STANDARD; PRT; 457 AA.
AC Q91085;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal polypeptide receptor precursor (VIP-R) (VIP
DE receptor).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND
RP INDUCTION.
RC TISSUE=Pituitary, and Small intestine;
RX MEDLINE=21560659; PubMed=11703071;
RA You S., Hsu C.-C., Kim H., Kho Y., Choi Y.J., el Halawani M.E.,
RA Farris J., Foster D.N.;
RA "Molecular cloning and expression analysis of the turkey vasoactive
RT intestinal peptide receptor.";
RL Gen. Comp. Endocrinol. 124:53-65 (2001).
RN [2]
RP SEQUENCE OF 198-457 FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96206340; PubMed=8618952;
RA Xu M., Proudhon J.A., Pitts G.R., Wong E.A., Foster D.N.,
RA el Halawani M.E.;
RT "Vasoactive intestinal peptide stimulates prolactin mRNA expression
RT in turkey pituitary cells: effects of dopaminergic drugs.";
RL Proc. Soc. Exp. Biol. Med. 212:52-62 (1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in pituitary, hypothalamus, small
CC intestine and ovarian follicles.
CC -!- DEVELOPMENTAL STAGE: Pituitary levels are highest in
CC nonphotostimulated and incubating birds and lower in
CC photostimulated, laying and photorefractory birds.
CC -!- INDUCTION: Pituitary levels decrease on VIP immunization.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

```

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U31991; AAA99740.2; --
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR000249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G-PROTEIN RECP F2_1; 1.
CC PROSITE; PS00650; G-PROTEIN RECP F2_2; 1.
CC PROSITE; PS0227; G-PROTEIN RECP F2_3; 1.
CC PROSITE; PS0261; G-PROTEIN RECP F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 457 VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR.
FT DOMAIN 20 141 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 142 166 1 (POTENTIAL).
FT DOMAIN 167 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 193 2 (POTENTIAL).
FT DOMAIN 194 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 239 3 (POTENTIAL).
FT DOMAIN 240 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 275 4 (POTENTIAL).
FT DOMAIN 276 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 316 5 (POTENTIAL).
FT DOMAIN 317 341 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 342 361 6 (POTENTIAL).
FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 393 7 (POTENTIAL).
FT DOMAIN 394 457 CYTOPLASMIC (POTENTIAL).
FT DISULFID 214 284 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 457 AA; 52769 MW; D862F1F2BE4ECB8C CRC64;

Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
Db |||||
169 LHCTRNVIHMLF 181

RESULT 15
ID VIPR PIG STANDARD; PRT; 458 AA.
AC Q28992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vasoactive intestinal polypeptide receptor I precursor (VIP-R-1)
DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
DE (PACAP type II receptor) (PACAP-R-2).
GN VIPR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsiung H.M., Smith D.P., Hyslop P.A., Heiman M.L., Hassan H.A.,
RA Zhang X.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL

```



```

DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G-PROTEIN RECP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN RECP_F2_2; 1.
DR PROSITE; PS0227; G-PROTEIN RECP_F2_3; 1.
DR PROSITE; PS0261; G-PROTEIN RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
FT DOMAIN 19 135 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 136 158 1 (POTENTIAL).
FT DOMAIN 159 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 186 2 (POTENTIAL).
FT DOMAIN 187 214 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 239 3 (POTENTIAL).
FT DOMAIN 240 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 275 4 (POTENTIAL).
FT DOMAIN 276 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 316 5 (POTENTIAL).
FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 339 359 6 (POTENTIAL).
FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 375 395 7 (POTENTIAL).
FT DOMAIN 396 462 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 462 AA; 52918 MW; D7A6204BCB9BB688 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHM 181
DB 159 FRLHCTRYNIHM 171
|||||
|||||

RESULT 19
GIPR_HUMAN STANDARD; PRT; 466 AA.
AC P48546; Q14401; Q16400;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gastric inhibitory polypeptide receptor precursor (GIP-R) (Glucose-
DE dependent insulinotropic polypeptide receptor).
GN GIPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RA Usdin T.B., Gruber C., Modi W., Bonner T.I.;
RL Submitted (0CT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=96013879; PubMed=7599426;
RA Volz A., Goke R., Lankat-Buttgereit B., Fehmann H.C., Bode H.P.,
RA Goke B.;
RT "Molecular cloning, functional expression, and signal transduction of
RT the GIP-receptor cloned from a human insulinoma.";
RL FEBS Lett. 373:23-29(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Pancreas;
RX MEDLINE=96007224; PubMed=7556958;
RA Gremlich S., Porret A., Hani E.H., Cherif D., Vionnet N., Froguel P.,
RA Thorens B.;

```

```

RT *Cloning, functional expression, and chromosomal localization of the
RT human pancreatic islet glucose-dependent insulinotropic polypeptide
RT receptor.*;
RL Diabetes 44:1202-1208(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=96121393; PubMed=8575774;
RA Yamada Y., Hayami T., Nakamura K., Kaisaki P.J., Someya Y.,
RA Wang C.Z., Seino S., Seino Y.;
RT "Human gastric inhibitory polypeptide receptor: cloning of the gene
RT (GIPR) and cDNA.*;
RL Genomics 29:773-776(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viewanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stiilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Brier A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 1.9 Mb region in 19ql3.2 between APOE and
RT D19S412.*;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Short;
CC IsoID=P48546-1; Sequence=Displayed;
CC Name=Long;
CC IsoID=P48546-2; Sequence=VSP_002002;
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U39231; A384418.1; -
CC EMBL; S79852; A3835419.2; -
CC EMBL; X61832; CAA57426.1; -
CC EMBL; D49559; BAA08503.1; -
CC EMBL; D49556; BAA08503.1; JOINED.
CC EMBL; D49557; BAA08503.1; JOINED.
CC EMBL; D49558; BAA08503.1; JOINED.
CC EMBL; AC006132; AAC97984.1; -
CC PIR; G02234; G02234.
CC PIR; S66676; S66676.
CC Genew; HGNC:4271; GIPR.
CC MIM; 137241; -
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0007190; P:adenylate cyclase activation; TAS.
CC GO; GO:0006091; P:energy pathways; TAS.
CC GO; GO:0007584; P:nutritional response pathway; TAS.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G-PROTEIN RECP_F2_1; 1.
CC PROSITE; PS00650; G-PROTEIN RECP_F2_2; 1.
CC PROSITE; PS0227; G-PROTEIN RECP_F2_3; 1.
CC PROSITE; PS0261; G-PROTEIN RECP_F2_4; 1.
CC PROSITE; PS0261; G-PROTEIN RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

```

KW Alternative splicing; Polymorphism.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 466 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT DOMAIN 22 138 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 139 161 1 (POTENTIAL).
 FT DOMAIN 162 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 170 189 2 (POTENTIAL).
 FT DOMAIN 190 217 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 218 242 3 (POTENTIAL).
 FT DOMAIN 243 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 278 4 (POTENTIAL).
 FT DOMAIN 279 293 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 294 319 5 (POTENTIAL).
 FT DOMAIN 320 341 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 342 362 6 (POTENTIAL).
 FT DOMAIN 363 377 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 378 398 7 (POTENTIAL).
 FT DOMAIN 399 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 77 V -> VGRDPAAPALWRRRTAPPLSAIVSQV (in isoform Long).
 FT VARSPLIC 399 399 /FTid=VSP_002002.
 FT VARIANT 207 207 A -> V (IN dBSNP:1800436).
 FT VARIANT 262 262 L -> V (IN dBSNP:5392).
 FT VARIANT 354 354 E -> Q (IN dBSNP:1800437).
 FT CONFLICT 12 12 /FTid=VAR_011810.
 FT CONFLICT 104 104 R -> G (IN REF. 2).
 FT CONFLICT 117 117 G -> R (IN REF. 2).
 FT CONFLICT 337 337 MISSING (IN REF. 3).
 FT CONFLICT 367 371 L -> V (IN REF. 2).
 FT CONFLICT 371 371 GALRF -> APCV (IN REF. 3).
 SQ SEQUENCE 466 AA; 53156 MW; CA5CF86BA0E32383 CRC64;
 Query Match 2.2%; Score 12; DB 1; Length 466;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 FRLHCTRNVIH 180
 Db 162 FRLHCTRNVIH 173
 RESULT 20
 GLR_HUMAN STANDARD; PRT; 477 AA.
 AC P47871;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon receptor precursor (GL-R).
 GN GCGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP TSUVE=Liver;
 RC SEQUENCE FROM N.A.
 RX MEDLINE-94121651; PubMed=7507321;
 RA Macneil D.J., Occi J.L., Hey P.J., Strader C.D., Graziano M.P.;
 RT "Cloning and expression of a human glucagon receptor."
 RL Biochem. Biophys. Res. Commun. 198:328-334(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-9412999; PubMed=8144028;
 RA Lok S., Kujiiper J.B., Jelinek L.J., Kramer J.M., Whitmore T.E.,
 RA Sprecher C.A., Mathews S., Grant F.J., Biggs S.H., Rosenberg G.B.;
 RT "The human glucagon receptor encoding gene: structure, cDNA sequence
 and chromosomal localization."
 RL Gene 140:203-209(1994).

RN SEQUENCE OF 21-54 FROM N.A.
 RP TISSUE=Placenta;
 RX MEDLINE=9429224; PubMed=8020989;
 RA Menzel S., Stoffel M., Espinosa R. III, Fernald A.A., Le Beau M.M.,
 RA Bell G.I.;
 RT "Localization of the glucagon receptor gene to human chromosome band
 17q25.";
 RL Genomics 20:327-328(1994).
 [4]
 RN VARIANT SER-40.
 RX MEDLINE=96034210; PubMed=7589886;
 RA Fujisawa T., Ikegami H., Yamato E., Takekawa K., Nakagawa Y.,
 RA Hamada Y., Ueda H., Fukuda M., Ogiwara T.;
 RT "A mutation in the glucagon receptor gene (Gly40Ser): heterogeneity
 in the association with diabetes mellitus.";
 RL Diabetologia 38:983-985(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
 CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
 CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DISEASE: IT IS A CANDIDATE FOR CERTAIN DEFECTS IN NON-INSULIN-
 CC DEPENDENT DIABETES MELLITUS (NIDDM). THE VARIANT IN POSITION 40
 CC (SER) IS FOUND IN SOME NIDDM PATIENTS, BUT ALSO IN NONDIABETIC
 CC SUBJECTS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U03469; AAC52063.1; -;
 CC EMBL; L20316; AAA53628.1; -;
 CC EMBL; L24751; AAA35897.1; -;
 CC PIR; JC2041; JC2041.
 CC Genew; HGNC:4192; GCGR.
 CC MIM; 138033; -;
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0004967; F:glucagon receptor activity; TAS.
 CC GO; GO:0006091; P:energy pathways; TAS.
 CC GO; GO:0007188; P:G-protein signaling, coupled to CAMP nucleo. . .; TAS.
 CC GO; GO:0007584; P:nutritional response pathway; TAS.
 CC GO; GO:0008217; P:regulation of blood pressure; TAS.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR01879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Polymorphism; Diabetes mellitus.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 477 GLUCAGON RECEPTOR.
 FT DOMAIN 26 142 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 143 166 1 (POTENTIAL).
 FT DOMAIN 167 173 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 174 193 2 (POTENTIAL).
 FT DOMAIN 194 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 3 (POTENTIAL).
 FT DOMAIN 250 263 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 264 285 4 (POTENTIAL).


```

FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 326 5 (POTENTIAL).
FT DOMAIN 327 350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 351 381 6 (POTENTIAL).
FT DOMAIN 370 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 404 7 (POTENTIAL).
FT DOMAIN 405 477 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 40 40 G -> S (IN dbSNP:1801483).
FT VARIANT 114 114 P -> A (IN dbSNP:5385).
FT SEQUENCE 477 AA; 54009 MW; ADBB477C6267AE6E CRC64;

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 255 LVEGLYLHNL 264
DB 243 LVEGLYLHNL 252

RESULT 21
ID GLP2 RAT STANDARD; PRT; 550 AA.
AC Q9Z0W0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glucagon-like peptide 2 receptor precursor (GLP-2 receptor) (GLP-2-R)
DE (GLP-2R).
GN GLP2R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN:Sprague-Dawley; TISSUE:Hypothalamus;
RX MEDLINE=99145591; PubMed=9990065;
RA Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
RA Demchshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
RA Summer-Smith M., Drucker D.J., Crivici A.;
RT "Prototypic G protein-coupled receptor for the intestinotrophic factor
RT glucagon-like peptide 2";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF105368; AAD16896.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
CC PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

```

```

DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 1 POTENTIAL.
FT CHAIN ? 550 GLUCAGON-LIKE PEPTIDE 2 RECEPTOR.
FT DOMAIN ? 179 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 202 1 (POTENTIAL).
FT DOMAIN 203 210 2 (POTENTIAL).
FT TRANSMEM 211 230 2 (POTENTIAL).
FT DOMAIN 231 261 3 (POTENTIAL).
FT TRANSMEM 262 286 3 (POTENTIAL).
FT DOMAIN 287 298 4 (POTENTIAL).
FT TRANSMEM 299 322 4 (POTENTIAL).
FT DOMAIN 323 337 5 (POTENTIAL).
FT TRANSMEM 338 363 5 (POTENTIAL).
FT DOMAIN 364 385 6 (POTENTIAL).
FT TRANSMEM 386 406 6 (POTENTIAL).
FT DOMAIN 407 421 7 (POTENTIAL).
FT TRANSMEM 422 442 7 (POTENTIAL).
FT DOMAIN 443 550 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 63102 MW; 22E269F81E25226 CRC64;

Query Match 1.8%; Score 10; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHM 181
DB 206 LHCTRNVIHM 215

RESULT 22
ID GLP2 HUMAN STANDARD; PRT; 553 AA.
AC O95838;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glucagon-like peptide 2 receptor precursor (GLP-2 receptor) (GLP-2-R)
DE (GLP-2R).
GN GLP2R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Stomach;
RA MEDLINE=99145591; PubMed=9990065;
RA Munroe D.G., Gupta A.K., Kooshesh F., Vyas T.B., Rizkalla G., Wang H.,
RA Demchshyn L., Yang Z.-H., Kamboj R.K., Chen H., McCallum K.,
RA Summer-Smith M., Drucker D.J., Crivici A.;
RT "Prototypic G protein-coupled receptor for the intestinotrophic factor
RT glucagon-like peptide 2";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1569-1574(1999).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 2. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF105367; AAD16895.1; -.

```



```

RESULT 24
VIPS RAT
ID VIPS RAT STANDARD; PRT; 437 AA.
AC P35000;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2)
DE (Pituitary adenylate cyclase activating polypeptide type III receptor)
DE (PACAP type III receptor) (PACAP-R-3).
GN VIPR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Olfactory bulb;
RX MEDLINE=94039806; PubMed=8224221;
RA Lutz E.-M., Sheward W.J., West K.M., Morrow J.A., Fink G.,
RA Harmar A.J.;
RT "The VIP2 receptor: molecular characterisation of a cDNA encoding a
RT novel receptor for vasoactive intestinal peptide.";
RL FEBS Lett. 334:3-8(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=95080140; PubMed=7988457;
RA Urdin T.B., Bonner T.I., Mezey E.;
RT "Two receptors for vasoactive intestinal polypeptide with similar
RT specificity and complementary distributions.";
RL Endocrinology 135:2662-2680(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; Z25885; CAA81104.1; -;
DR EMBL; U09631; AAB60459.1; -;
DR PIR; S39069; S39069.
DR InterPro; IPR000832; GPCR secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS02611; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE; PS02611; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 2.
FT DOMAIN 23 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 150 1 (POTENTIAL).
FT DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 158 177 2 (POTENTIAL).
FT DOMAIN 178 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 226 3 (POTENTIAL).
FT DOMAIN 227 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 261 4 (POTENTIAL).

```

```

FT DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302 5 (POTENTIAL).
FT DOMAIN 303 327 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 328 347 6 (POTENTIAL).
FT DOMAIN 348 359 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 360 379 7 (POTENTIAL).
FT DOMAIN 380 437 CYTOPLASMIC (POTENTIAL).
FT DISULFID 201 270 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 383 383 C -> R (IN REF. 2).
SQ SEQUENCE 437 AA; 49552 MW; 7E10218A9EE31360 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNYIH 180
DB 153 LHCTRYNYIH 161
|||||
|||||

RESULT 25
VIPS_HUMAN
ID VIPS_HUMAN STANDARD; PRT; 438 AA.
AC P41587; Q15870;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vasoactive intestinal polypeptide receptor 2 precursor (VIP-R-2)
DE (Pituitary adenylate cyclase activating polypeptide type III receptor)
DE (PACAP type III receptor) (PACAP-R-3) (Helodermin-preferring VIP
DE receptor).
GN VIPR2 OR VIP2R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95110300; PubMed=7811244;
RA Svoboda M., Tastenoy M., van Rampelbergh J., Goossens J.-F., Neef P.,
RA Waelbroeck M., Robberecht P.;
RT "Molecular cloning and functional characterization of a human VIP
RT receptor from SUP-T1 lymphoblasts.";
RL Biochem. Biophys. Res. Commun. 205:1617-1624(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97092885; PubMed=8938447;
RA Mackay M., Fantes J., Scherer S., Boyle S., West K., Tsui L.C.,
RA Belloni E., Lutz E., van Heyningen V., Harmar A.J.;
RT "Chromosomal localization in mouse and human of the vasoactive
RT intestinal peptide receptor type 2 gene: a possible contributor to
RT the holoprosencephaly 3 phenotype.";
RL Genomics 37:345-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=97087354; PubMed=8933357;
RA Wei Y., Mojsov S.;
RT "Tissue specific expression of different human receptor types for
RT pituitary adenylate cyclase activating polypeptide and vasoactive
RT intestinal polypeptide: implications for their role in human
RT physiology.";
RL J. Neuroendocrinol. 8:811-817(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99412192; PubMed=10481065;
RA Lutz E.M., Shen S., Mackay M., West K., Harmar A.J.;
RT "Structure of the human VIP2R gene for vasoactive intestinal peptide
RT type 2 receptor.";
RL FEBS Lett. 458:197-203(1999).

```

RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Matek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE ADENYLYL CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; LA0764; AAC41756.1; -
 DR EMBL; L36566; AAC37569.1; -
 DR EMBL; X95097; CAA64474.1; -
 DR EMBL; U18810; AAC50872.1; -
 DR EMBL; Y18423; CAB41899.1; -
 DR EMBL; Y18424; CAB41899.1; JOINED.
 DR EMBL; Y18425; CAB41899.1; JOINED.
 DR EMBL; Y18426; CAB41899.1; JOINED.
 DR EMBL; Y18427; CAB41899.1; JOINED.
 DR EMBL; Y18428; CAB41899.1; JOINED.
 DR EMBL; Y18430; CAB41899.1; JOINED.
 DR EMBL; Y18431; CAB41899.1; JOINED.
 DR EMBL; BC010569; AAH10569.1; -
 DR PIR; G02822; G02822.
 DR Genew; HGNC:12695; VIPR2.
 DR MIM; 601970; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECIP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECIP_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECIP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECIP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Polymorphism.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 438 VASOACTIVE INTESTINAL POLYPEPTIDE

FT DOMAIN 24 126
 FT TRANSMEM 127 151
 FT DOMAIN 152 158
 FT TRANSMEM 159 178
 FT DOMAIN 179 203
 FT TRANSMEM 204 227
 FT DOMAIN 228 240
 FT TRANSMEM 241 262
 FT DOMAIN 263 279
 FT TRANSMEM 280 303
 FT DOMAIN 304 328
 FT TRANSMEM 329 348
 FT DOMAIN 349 360
 FT TRANSMEM 361 380
 FT DOMAIN 381 438
 FT DISULFID 202 271
 FT CARBOHYD 58 58
 FT CARBOHYD 88 88
 FT CARBOHYD 92 92
 FT VARIANT 39 39
 FT VARIANT 412 412
 FT CONFLICT 424 424
 FT SEQUENCE 438 AA; 49478 MW; 265A43A70BE09699 CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 438;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 172 LHCTRYNVIH 180
 DB 154 LHCTRYNVIH 162
 RESULT 26
 GLPI_HUMAN STANDARD; PRT; 463 AA.
 ID AC P43270; Q99669;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
 DE (GLP-1R).
 GN GLP1R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancratic islets;
 RX MEDLINE=94009966; PubMed=8405712;
 RA Thorens B., Porret A., Buehler L., Deng S., Morel P., Widmann C.;
 RT "Cloning and functional expression of the human islet GLP-1 receptor.
 RT Demonstration that exendin-4 is an agonist and exendin-(9-39) an
 RT antagonist of the receptor.";
 RL Diabetes 42:1678-1682 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=94008746; PubMed=8404634;
 RA Dillon J.S., Tanizawa Y., Wheeler M.B., Leng X., Ligon B.B.,
 RA Rabin D.U., Yoo-Warren H., Permutt M., Boyd A.E.;
 RT "Cloning and functional expression of the human glucagon-like
 RT peptide-1 (GLP-1) receptor.";
 RL Endocrinology 133:1907-1910 (1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
 RC TISSUE=Gastric carcinoma;
 RX MEDLINE=94029985; PubMed=8216285;
 RA Graziano M.P., Hey P.J., Borzkowski D., Chicchi G.C., Strader C.D.;

RT "Cloning and functional expression of a human glucagon-like peptide-1
receptor.";
RL Biochem. Biophys. Res. Commun. 196:141-146(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Insulinoma; PubMed=7517895;
RX MEDLINE=94298957; PubMed=7517895;
RA van Eyll B., Lankat-Buttgereit B., Bode H.P., Goetze R., Goetze B.;
RT "Signal transduction of the GLP-1-receptor cloned from a human
insulinoma.";
RL FEBS Lett. 348:7-13(1994).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RC TISSUE=Pancreas;
RX MEDLINE=95145713; PubMed=7843404;
RA Wei Y., Moysov S.;
RT "Tissue-specific expression of the human receptor for glucagon-like
peptide-1: brain, heart and pancreatic forms have the same deduced
amino acid sequences.";
RL FEBS Lett. 358:219-224(1995).
RN [6]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RT Tsubuni S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A., AND VARIANT LEU-260.
RA Smalley C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 1-26 FROM N.A.
RC TISSUE=Placenta;
RA Lankat-Buttgereit B., Goetze B.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U01104; AAA03614.1; -;
CC EMBL; U01157; AAC62471.1; -;
CC EMBL; U01156; AAC50050.1; -;
CC EMBL; U23503; AAA17021.1; -;
CC EMBL; U10037; AAA63787.1; -;
CC EMBL; AB065685; BAC05908.1; -;
CC EMBL; AL035690; CAB71177.1; -;
CC EMBL; U6062; AAB64013.1; -;
CC PIR; I84494; I84494.
CC PIR; S71624; S71624.
CC Genew; HGNC:4324; GLP1R.
CC MIM; 138032; -;
CC GO; GO:0016021; C:integral to membrane; TAS.
CC DR; GO; GO:0005886; C:plasma membrane; TAS.
CC DR; GO; GO:0007190; P:adenylate cyclase activation; TAS.
CC DR; InterPro; IPR000832; GPCR_secretin.
CC DR; Pfam; PF00002; 7tm_2; 1.
CC DR; Pfam; PF02793; HRM; 1.
CC DR; PRINTS; PR00249; GPCRSECRETIN.
CC DR; SMART; SM00008; Hormn; 1.
CC DR; PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC DR; PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Polymorphism.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 463 GLUCAGON-LIKE PEPTIDE 1 RECEPTOR.
FT DOMAIN 24 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 168 1 (POTENTIAL).
FT DOMAIN 169 176 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 196 2 (POTENTIAL).
FT DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 252 3 (POTENTIAL).
FT DOMAIN 253 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 288 4 (POTENTIAL).
FT DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 329 5 (POTENTIAL).
FT DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 6 (POTENTIAL).
FT DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 388 408 7 (POTENTIAL).
FT DOMAIN 409 463 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 260 P -> L.
FT /FTID=VAR 015098.
FT CONFLICT 12 12 L -> V (IN REF. 1, 4 AND 7).
FT CONFLICT 136 137 SP -> WG (IN REF. 1).
FT CONFLICT 137 137 P -> R (IN REF. 4).
FT CONFLICT 151 151 G -> A (IN REF. 1).
FT CONFLICT 221 221 Q -> L (IN REF. 5).
FT CONFLICT 289 289 Y -> I (IN REF. 1).
FT CONFLICT 316 316 A -> G (IN REF. 2).
SQ SEQUENCE 463 AA; 53059 MW; 04DB63C58E54DD55 CRC64;
Query Match 1.7%; Score 9; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 172 LHCTRNVIH 180
Db 172 LHCTRNVIH 180
RESULT 27
GLP1_RAT
ID GLP1_RAT STANDARD; PRT; 463 AA.
AC P32301; Q64073;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
DE (GLP-1R).
GN GLP1R OR GLPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=92409572; PubMed=1326760;
RA Thorens B.;
RT "Expression cloning of the pancreatic beta cell receptor for the
RT glucocorticoid hormone glucagon-like peptide 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:8641-8645(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
EX MEDLINE=95112989; PubMed=7813606;
RA Lankat-Buttgereit B., Goke R., Fehmann H.C., Richter G., Goke B.;
RT "Molecular cloning of a cDNA encoding for the GLP-1 receptor
RT expressed in rat lung.";

RL Exp. Clin. Endocrinol. 102:341-347(1994).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE

CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH

CC ACTIVATE ADENYLATE CYCLASE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: PANCREATIC ISLETS, STOMACH, LUNG, RAT

CC INSULINOMA CELL LINE.

CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; M97797; AAA73377.1; -.

CC EMBL; S75952; -; NOT ANNOTATED_CDS.

CC PIR; A46172; A46172; GPCR_secretin.

CC InterPro; IPR000832; GPCR_secretin.

CC Pfam; PF00002; 7tm_2; 1.

CC Pfam; PF02793; HRM; 1.

CC PRINTS; PR00249; GPCRSSECRETIN.

CC SMART; SM00008; Hormr; 1.

CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

CC PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.

CC PROSITE; PS00652; G_PROTEIN_RECEP_F2_4; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.

CC SIGNAL 1 21 POTENTIAL.

CC CHAIN 22 463 GLUCAGON-LIKE PEPTIDE 1 RECEPTOR.

CC DOMAIN 22 145 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 146 168 1 (POTENTIAL).

CC DOMAIN 169 176 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 177 196 2 (POTENTIAL).

CC DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 228 252 3 (POTENTIAL).

CC DOMAIN 253 264 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 265 288 4 (POTENTIAL).

CC DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 304 329 5 (POTENTIAL).

CC DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 352 372 6 (POTENTIAL).

CC DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 388 408 7 (POTENTIAL).

CC DOMAIN 409 463 CYTOPLASMIC (POTENTIAL).

CC CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CONFLICT 323 323 V -> I (IN REF. 2).

CC SEQUENCE 463 AA; 52876 MW; ABE21838EBE621F CRC64;

Query Match 1.78; Score 9; DB 1; Length 463;

Best Local Similarity 100.0%; Pred. No. 0.58; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

Qy 172 LHCTRNVIH 180

Db 172 LHCTRNVIH 180

RESULT 28

PACR HUMAN

ID_PACR HUMAN STANDARD; PRT; 468 AA.

AC P41586;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type I receptor

DE precursor (PACAP type I receptor) (PACAP-R-1).

GN ADCYAP1R1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pituitary;

RX MEDLINE=94071918; PubMed=7902709;

RA Ogi K., Miyamoto Y., Masuda Y., Habata Y., Hosoya M., Ohtaki T.,

RA Masuo Y., Onda H., Fujino M.;

RT "Molecular cloning and functional expression of a cDNA encoding a

RT human pituitary adenylate cyclase activating polypeptide receptor.";

RL Biochem. Biophys. Res. Commun. 196:1511-1521(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Pituitary;

RX MEDLINE=95154842; PubMed=7851900;

RA Stoffel M., Espinosa R., Trabb J.B., le Beau M.M., Bell G.I.;

RT "Human type I pituitary adenylate cyclase activating polypeptide

RT receptor (ADCYAP1R): localization to chromosome band 7p14 and

RT integration into the cytogenetic, physical and genetic map of

RT chromosome 7.";

RL Genomics 23:697-699(1994).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE

CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE

CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,

CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND

CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM

CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE

CC GASTROINTESTINAL TRACT.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN THE BRAIN, LOW EXPRESSION IN

CC THE LUNG, LIVER, THYMUS, SPLEEN, PANCREAS AND PLACENTA.

CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; D17516; BAA04466.1; ALT INIT.

CC EMBL; AB065700; BAC05923.1; -.

CC EMBL; U09216; AAA19323.1; -.

CC Genew; HGNC:242; ADCYAP1R1.

CC MIM; 102981; -.

CC GO; GO:0005887; C:integral to plasma membrane; TAS.

CC GO; GO:0004872; F:receptor activity; TAS.

CC InterPro; IPR000832; GPCR_secretin.

CC InterPro; IPR001879; hormn_receptor.

CC Pfam; PF00002; 7tm_2; 1.

CC Pfam; PF02793; HRM; 1.

CC PRINTS; PR00249; GPCRSSECRETIN.

CC SMART; SM00008; Hormr; 1.

CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

CC PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.

CC PROSITE; PS00652; G_PROTEIN_RECEP_F2_4; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

CC Spermatoogenesis.

CC SIGNAL 1 20 POTENTIAL.

CC CHAIN 21 468 PITUITARY ADENYLATE CYCLASE ACTIVATING

CC POLYPEPTIDE TYPE I RECEPTOR.

CC DOMAIN 21 155 EXTRACELLULAR (POTENTIAL).

```
FT TRANSMEM 156 178 1 (POTENTIAL).
FT DOMAIN 179 186 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 187 205 2 (POTENTIAL).
FT DOMAIN 206 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 253 3 (POTENTIAL).
FT DOMAIN 254 268 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 269 291 4 (POTENTIAL).
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 332 5 (POTENTIAL).
FT DOMAIN 333 350 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 351 371 6 (POTENTIAL).
FT DOMAIN 372 385 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 386 405 7 (POTENTIAL).
FT DOMAIN 406 468 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 468 AA; 53313 MW; BB515B84E9F28977 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.59; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 183 LFVSEMLRA 191
| | | | |
Db 192 LFVSEMLRA 200

RESULT 29
GLR_MOUSE
ID GLR_MOUSE STANDARD; PRT; 485 AA.
AC O61506; Q63960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucagon receptor precursor (GL-R).
GN GCGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069600; PubMed=7590348;
EA Burcein R., Li J., Charron M.J.;
RT "Cloning and sequence analysis of the murine glucagon receptor-
encoding gene.";
RL Gene 164:305-310(1995).
RN [2]
RP SEQUENCE OF 324-458 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94208442; PubMed=8156917;
RA Campos R.V., Lee Y.C., Drucker D.J.;
RT "Divergent tissue-specific and developmental expression of receptors
for glucagon and glucagon-like peptide-1 in the mouse.";
RL Endocrinology 134:2156-2164(1994).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LIVER, KIDNEY,
CC ADRENAL, LUNG AND STOMACH, WHILE LOWER LEVELS OF EXPRESSION ARE
CC DETECTED IN BROWN AND WHITE ADIPOSE TISSUE, CEREBELLUM, DUODENUM
CC AND HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

```
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L38613; AAA88244.1; -.
DR EMBL; S69384; AAB30529.2; -.
DR PIR; JC4363; JC4363.
DR MGD; MGI:99572; GCGR.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS02027; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS02061; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE; PS02061; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 485 GLUCAGON RECEPTOR.
FT DOMAIN 27 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167 1 (POTENTIAL).
FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194 2 (POTENTIAL).
FT DOMAIN 195 226 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 227 250 3 (POTENTIAL).
FT DOMAIN 251 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 286 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 287 304 4 (POTENTIAL).
FT TRANSMEM 305 327 5 (POTENTIAL).
FT DOMAIN 328 351 6 (POTENTIAL).
FT TRANSMEM 352 370 7 (POTENTIAL).
FT DOMAIN 371 382 8 (POTENTIAL).
FT TRANSMEM 383 405 9 (POTENTIAL).
FT DOMAIN 406 485 10 (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 325 325 H -> R (IN REF. 2).
FT CONFLICT 328 328 Q -> H (IN REF. 2).
SQ SEQUENCE 485 AA; 54872 MW; 27724574412EB9BA CRC64;

Query Match 1.7%; Score 9; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIH 180
| | | | |
Db 170 LHCTRNVIH 178

RESULT 30
GLR_RAT
ID GLR_RAT STANDARD; PRT; 485 AA.
AC P30082;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glucagon receptor precursor (GL-R).
GN GCGR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93206096; PubMed=8384375;
```

RA Jelinek L.J., Lok S., Grant F.J., Rosenberg G.B., Smith R.A.,
 RA Benesch P.A., Sheppard P.O., O'Hara P.J., Foster D.C.,
 RA Kuiper J.L., Biggs S.H., Walker K.M., Chen L.H., McKernan P.A.,
 RA Kindsvogel W.;
 RT "Expression cloning and signaling properties of the rat glucagon
 RT receptor.";
 RL Science 259:1614-1616(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93213282; PubMed=8384842;
 RA Svoboda M., Ciccarelli E., Tastenoy M., Cauvin A., Stievenart M.,
 RA Christophe J.;
 RT "Small introns in a hepatic cDNA encoding a new glucagon-like peptide
 RT 1-type receptor.";
 RL Biochem. Biophys. Res. Commun. 191:479-486(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=94364484; PubMed=8082779;
 RA Maget B., Tastenoy M., Svoboda M.;
 RT "Sequencing of eleven introns in genomic DNA encoding rat glucagon
 RT receptor and multiple alternative splicing of its mRNA.";
 RL FEBS Lett. 351:271-275(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
 CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
 CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L04796; AAA16439.1; -
 CC EMBL; X68692; AAA48651.1; -
 CC EMBL; M96674; AAA02392.1; -
 CC EMBL; U63021; AAB16800.1; -
 CC PIR; JQ1957; JQ1957.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm.2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 CC PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 26
 FT CHAIN 27 485
 FT DOMAIN 27 143
 FT TRANSMEM 144 167
 FT DOMAIN 168 174
 FT TRANSMEM 175 194
 FT DOMAIN 195 226
 FT TRANSMEM 227 250
 FT DOMAIN 251 264
 FT TRANSMEM 265 286
 FT DOMAIN 287 304
 FT TRANSMEM 305 327
 FT DOMAIN 328 351
 FT TRANSMEM 352 370
 FT DOMAIN 371 382
 FT TRANSMEM 383 405
 FT DOMAIN 406 485

FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 216 216 W -> C (IN REF. 2).
 FT CONFLICT 324 324 V -> A (IN REF. 2).
 SQ SEQUENCE 485 AA; 55038 MW; 91AC67D7A4F5090E CRC64;
 Query Match 1.7%; Score 9; DB 1; Length 485;
 Best Local Similarity 100.0%; Pred.No. 0.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 172 LHCTRNVIH 180
 Db 170 LHCTRNVIH 178
 RESULT 31
 GLP1_MOUSE
 ID GLP1_MOUSE STANDARD; PRT; 489 AA.
 AC O35659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucagon-like peptide 1 receptor precursor (GLP-1 receptor) (GLP-1-R)
 DE (GLP-1R).
 GN GLP1R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=98227650; PubMed=9568699;
 RA Flamez D., van Breusegem A., Scrocchi L.A., Quartier E., Pipeleers D.,
 RA Drucker D.J., Shuit F.;
 RT "Mouse pancreatic beta-cells exhibit preserved glucose competence
 RT after disruption of the glucagon-like peptide-1 receptor gene.";
 RL Diabetes 47:646-652(1998).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON-LIKE PEPTIDE 1. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE ADENYLYL CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ001692; CAA04930.1; -
 CC MGD; MGI:99571; Glplr.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm.2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 CC PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 21
 FT CHAIN 22 489
 FT DOMAIN 22 145
 FT TRANSMEM 146 168
 FT DOMAIN 169 176
 FT TRANSMEM 177 196


```

FT DOMAIN 197 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 252 3 (POTENTIAL).
FT DOMAIN 258 264 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 265 268 4 (POTENTIAL).
FT DOMAIN 289 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 329 5 (POTENTIAL).
FT DOMAIN 330 351 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 352 372 6 (POTENTIAL).
FT DOMAIN 373 387 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 388 408 7 (POTENTIAL).
FT DOMAIN 409 489 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 489 AA; 55878 MW; A859487F2D0ED041 CRC64;

Query Match 1.7%; Score 9; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIH 180
DB 172 LHCTRYIH 180
[1]|||||

RESULT 32
PACR MOUSE
ID PACR MOUSE STANDARD; PRT; 496 AA.
AC P70205;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCVAPR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96256640; PubMed=8664310;
RA Hashimoto H., Yamamoto K., Hagigara N., Ogawa N., Nishino A.,
RA Aino H., Nogi H., Imanishi K., Matsuda T., Baba A.;
RT "cDNA cloning of a mouse pituitary adenylate cyclase-activating
RT polypeptide receptor.";
RL Biochim. Biophys. Acta 1281:129-133 (1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D82935; BAA11639.1; -
CC MGD; MGI:108449; Adcvaprl.
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; HormR; 1.

```

```

DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
DR PROSITE; PS00650; G PROTEIN RECP F2_2; 1.
DR PROSITE; PS0227; G PROTEIN RECP F2_3; 1.
DR PROSITE; PS0261; G PROTEIN RECP F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Spermatogenesis.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 496 PITUITARY ADENYLATE CYCLASE ACTIVATING
FT DOMAIN 21 155 POLYPEPTIDE TYPE I RECEPTOR.
FT TRANSMEM 156 178 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 179 186 1 (POTENTIAL).
FT TRANSMEM 187 205 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 206 227 2 (POTENTIAL).
FT TRANSMEM 228 253 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 254 268 3 (POTENTIAL).
FT TRANSMEM 269 291 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 292 309 4 (POTENTIAL).
FT TRANSMEM 310 332 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 333 378 5 (POTENTIAL).
FT TRANSMEM 379 399 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 400 413 6 (POTENTIAL).
FT TRANSMEM 414 433 7 (POTENTIAL).
FT DOMAIN 434 496 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 496 AA; 56639 MW; 47B5D51D209060A CRC64;

Query Match 1.7%; Score 9; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSEMLRA 191
DB 192 LFVSEMLRA 200
[1]|||||

RESULT 33
PACR BOVIN
ID PACR BOVIN STANDARD; PRT; 513 AA.
AC Q29627;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide type I receptor
DE precursor (PACAP type I receptor) (PACAP-R-1).
GN ADCVAPR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Brain;
RX MEDLINE=94325336; PubMed=8049255;
RA Miyamoto Y., Habata Y., Ohtaki T., Masuda Y., Ogi K., Onda H.,
RA Fujino M.;
RT "Cloning and expression of a complementary DNA encoding the bovine
RT receptor for pituitary adenylate cyclase-activating polypeptide
RT (PACAP).";
RL Biochim. Biophys. Acta 1218:297-307 (1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE. MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
CC LUTEINIZING HORMONE, GROWTH HORMONE, PROLACTIN, EPINEPHRINE, AND
CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
CC GASTROINTESTINAL TRACT (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;

```


DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)
DE (Corticotropin-releasing hormone receptor 2) (CRH-R 2).
GN CRHR2 OR CRF2R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Hypothalamus, and Lung;
RX MEDLINE=95148632; PubMed=7846082;
RA Lovenberg T.W., Liaw C.W., Grigoriadis D.E., Clevenger W.,
RA Chalmers D.T., de Souza E.B., Oltersdorf T.;
RA Proc. Natl. Acad. Sci. U.S.A. 92:5759-5759(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY CRF BINDING. ALSO BINDS TO UROCORTIN I, II AND
CC III. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=CRF2-alpha;
CC IsoId=P47866-1; Sequence=Displayed;
CC Note=Major isoform;
CC Name=CRF2-beta;
CC IsoId=P47866-2; Sequence=VSP 002001;
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIMBIC REGIONS OF
CC THE BRAIN SUCH AS THE LATERAL SEPTUM, THE ENTORHINAL CORTEX, THE
CC HYPOTHALAMIC VENTROMEDIAL NUCLEUS AND SEVERAL AMYGDALOID NUCLEI.
CC ALSO DETECTABLE IN LUNG, KIDNEY AND HEART.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U16253; AAC52159.1; -.
CC PIR; A55610; A55610.
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM7; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Alternative splicing.
CC SIGNAL 1 17 POTENTIAL.
CC CHAIN 18 411 CORTICOTROPIN RELEASING FACTOR RECEPTOR
CC 2.
CC DOMAIN 18 118 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 119 139 1 (POTENTIAL).
CC DOMAIN 140 148 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 149 168 2 (POTENTIAL).
CC DOMAIN 169 185 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 186 209 3 (POTENTIAL).
CC DOMAIN 210 223 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 224 245 4 (POTENTIAL).

FT DOMAIN 246 264 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 265 287 5 (POTENTIAL).
FT DOMAIN 288 310 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 311 330 6 (POTENTIAL).
FT DOMAIN 331 345 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 346 365 7 (POTENTIAL).
FT DOMAIN 366 411 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 41 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 34 MDAALLSLRANSLALAEELLLDGWGEPPDPE -> MGH
FT PEGSLPSAQLLCVLLSLPLQLVAQGRPLQDQLMTLLEQY
FT CHRTTRNFS (in isoform CRF2-beta).
FT /FTId=VSP 002001.
SQ SEQUENCE 411 AA; 47706 MW; 1C6E85801BC94469 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 SFQGFVS 410
DB 349 SFQGFVS 356
RESULT 38
ID YPEB_SYN2 STANDARD; PRT; 411 AA.
AC P42784;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PETB 5'region (fragment).
OS Synchococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxId=32049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93043038; PubMed=1421151;
RA Brand S.N., Tan X., Widger W.R.;
RT "Cloning and sequencing of the petBD operon from the cyanobacterium
RT Synchococcus sp. PCC 7002.";
RL Plant Mol. Biol. 20:481-491(1992).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X63049; CAA44776.1; -.
CC MEROPS; S41.002; -.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR004447; Protease_Cterm.
CC InterPro; IPR003581; TSFC.
CC Pfam; PF00595; PDZ; 1.
CC SMART; SM00228; PDZ; 1.
CC SMART; SM00245; TSPC; 1.
CC TIGRFAMs; TIGR00225; prc; 1.
CC PROSITE; PS50106; PDZ; 1.
CC KW Hypothetical protein; Hydrolase; Serine protease.
FT DOMAIN 100 170 PDZ.
FT NON_TER 411 411
SQ SEQUENCE 411 AA; 45418 MW; B6FA904E2D7F551B CRC64;
Query Match 1.5%; Score 8; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 LVLVLVFG 373
 Db 15 LVLVLVFG 22

RESULT 39
 CRF2_XENLA STANDARD; PRT; 413 AA.
 ID CRF2_XENLA STANDARD; PRT; 413 AA.
 AC O42603;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)
 DE (Corticotropin-releasing hormone receptor 2) (CRH-R 2).
 GN CRF2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Heart;
 RX MEDLINE=97465573; PubMed=9326293;
 RA Dautzenberg F.M., Dietrich K., Balchaudhuri M.R., Spiess J.;
 RT "Identification of two corticotropin-releasing factor receptors from
 RT Xenopus laevis with high ligand selectivity: unusual pharmacology of
 RT the type 1 receptor.";
 RL J. Neurochem. 69:1640-1649 (1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
 CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y14037; CAA74364.1; --
 CC InterPro; IPR000832; GPCR_secretin.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM_1
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS00277; G_PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL 1 ?
 FT CHAIN ? 413 CORTICOTROPIN RELEASING FACTOR RECEPTOR
 FT 2.
 FT DOMAIN ? 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 141 1 (POTENTIAL).
 FT DOMAIN 142 150 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 151 170 2 (POTENTIAL).
 FT DOMAIN 171 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 211 3 (POTENTIAL).
 FT DOMAIN 212 225 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 226 247 4 (POTENTIAL).
 FT DOMAIN 248 266 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 267 289 5 (POTENTIAL).
 FT DOMAIN 290 312 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 313 332 6 (POTENTIAL).
 FT DOMAIN 333 347 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 348 367 7 (POTENTIAL).
 FT DOMAIN 368 413 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 413 AA; 48458 MW; DAD422FOA96C4626 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 413;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 SFQGFVVS 410
 Db 351 SFQGFVVS 358

RESULT 40
 CRF1_MOUSE STANDARD; PRT; 415 AA.
 ID CRF1_MOUSE STANDARD; PRT; 415 AA.
 AC P35347;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
 DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
 GN CRHR1 OR CRHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=94063063; PubMed=8243652;
 RA Vita N., Laurent P., Lefort S., Chalou P., Lelias J.-M., Kaghad M.,
 RA Le Fur G., Caput D., Ferrara P.;
 RT "Primary structure and functional expression of mouse pituitary and
 RT human brain corticotrophin releasing factor receptors.";
 RL FEBS Lett. 335:1-5 (1993).
 CC [2]
 CC SEQUENCES FROM N.A.
 CC STRAIN=ILS, and ISS;
 CC MEDLINE=21363810; PubMed=11471062;
 CC Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 CC Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 CC "High-throughput sequence identification of gene coding variants
 CC within alcohol-related QTLs.";
 CC Mamm. Genome 12:657-663 (2001).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, PITUITARY GLAND, TESTIS. NOT DETECTED
 CC IN PLACENTA, PERIPHERAL BLOOD, LYMPHOCYTES, KIDNEY AND LIVER.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X72305; CAA51053.1; --
 CC EMBL; AF483484; AAL90758.1; --
 CC EMBL; AF483485; AAL90759.1; --
 CC PIR; S39535; S39535.
 CC MGD; MGI:88498; Chrl1.
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.


```

FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 228 249 4 (POTENTIAL). (POTENTIAL).
FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 291 5 (POTENTIAL).
FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 315 334 6 (POTENTIAL).
FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 369 7 (POTENTIAL).
FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 30 54
FT DISULFID 44 87
FT DISULFID 68 102
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 415 AA; 47842 MW; 48D6704B31D4C013 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
Db 353 SFQGFVVS 360

RESULT 42
CRF1 SHEEP STANDARD; PRT; 415 AA.
AC Q62772;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRH1.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=99079328; PubMed=9863624;
RA Myers D.A., Trinh J.V., Myers T.R.;
RT "Structure and function of the ovine type 1 corticotropin releasing
RT factor receptor (CRF1) and a carboxyl-terminal variant.";
RL Mol. Cell. Endocrinol. 144:21-35(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF054582; AAC08027.1; .
CC InterPro; IPR000832; GPCR secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM1; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.

```

```

DR PROSITE; PS00649; G-PROTEIN RECEPTOR F2.1; FALSE_NEG.
DR PROSITE; PS00650; G-PROTEIN RECEPTOR F2.2; 1.
DR PROSITE; PS00651; G-PROTEIN RECEPTOR F2.3; 1.
DR PROSITE; PS00652; G-PROTEIN RECEPTOR F2.4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 415 CORTICOTROPIN RELEASING FACTOR RECEPTOR
FT DOMAIN 24 121 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 122 142 1 (POTENTIAL).
FT DOMAIN 143 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 171 2 (POTENTIAL).
FT DOMAIN 172 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 213 3 (POTENTIAL).
FT DOMAIN 214 227 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 228 249 4 (POTENTIAL).
FT DOMAIN 250 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 291 5 (POTENTIAL).
FT DOMAIN 292 314 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 315 334 6 (POTENTIAL).
FT DOMAIN 335 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 369 7 (POTENTIAL).
FT DOMAIN 370 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 30 54 BY SIMILARITY.
FT DISULFID 44 87 BY SIMILARITY.
FT DISULFID 68 102 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 47558 MW; FAS652D12B4CDC4 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
Db 353 SFQGFVVS 360

RESULT 43
CRF1 XENLA STANDARD; PRT; 415 AA.
AC Q42602;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRF1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97465573; PubMed=9326293;
RA Dautzenberg F.M., Dietrich K., Palchaudhuri M.R., Spiess J.;
RT "Identification of two corticotropin-releasing factor receptors from
RT Xenopus laevis with high ligand selectivity: unusual pharmacology of
RT the type 1 receptor.";
RL J. Neurochem. 69:1640-1649(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

```



```

CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y14036; CAA74363.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm.2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 415
FT FT
FT FT
FT DOMAIN 25 121
FT TRANSMEM 122 142
FT DOMAIN 143 151
FT TRANSMEM 152 171
FT DOMAIN 172 189
FT TRANSMEM 190 213
FT DOMAIN 214 227
FT TRANSMEM 228 249
FT DOMAIN 250 268
FT TRANSMEM 269 291
FT DOMAIN 292 314
FT TRANSMEM 315 334
FT DOMAIN 335 349
FT TRANSMEM 350 369
FT DOMAIN 370 415
FT DISULFID 30 54
FT DISULFID 44 87
FT DISULFID 68 102
FT CARBOHYD 38 38
FT CARBOHYD 45 45
FT CARBOHYD 78 78
FT CARBOHYD 90 90
FT CARBOHYD 90 90
SQ SEQUENCE 415 AA; 47786 MW; 74BD24C17907B74D CRC64;

Query Match 1.5%; Score 8; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SPQGFVVS 410
DB 353 SFQGFVVS 360
|||||

RESULT 44
ID_CRF1_CHICK STANDARD; PRT; 420 AA.
AC Q90512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=96107136; PubMed=8536612;
RA Yu J., Xie L.Y., Abou-Samra A.-B.;
RT "Molecular cloning of a type A chicken corticotropin-releasing factor
RT receptor with high affinity for urotensin I.",
RL Endocrinology 137:192-197(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY BINDING FOR UROTENSIN I. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -----
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41563; AAA96565.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm.2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 28
FT CHAIN 29 420
FT FT
FT FT
FT DOMAIN 29 126
FT TRANSMEM 127 147
FT DOMAIN 148 156
FT TRANSMEM 157 176
FT DOMAIN 177 194
FT TRANSMEM 195 218
FT DOMAIN 219 232
FT TRANSMEM 233 254
FT DOMAIN 255 273
FT TRANSMEM 274 296
FT DOMAIN 297 319
FT TRANSMEM 320 339
FT DOMAIN 340 354
FT TRANSMEM 355 374
FT DOMAIN 375 420
FT DISULFID 35 59
FT DISULFID 49 92
FT DISULFID 73 107
FT CARBOHYD 43 43
FT CARBOHYD 50 50
FT CARBOHYD 83 83
FT CARBOHYD 95 95
FT CARBOHYD 103 103
FT CARBOHYD 103 103
SQ SEQUENCE 420 AA; 48600 MW; 8C5C992925F62316 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
DB 358 SFQGFVVS 365
|||||

RESULT 45
ID_CRF2_MOUSE STANDARD; PRT; 431 AA.

```


AC Q60748; Q60783; Q60808;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Corticotropin releasing factor receptor 2 precursor (CRF-R 2) (CRF2)
DE (Corticotropin-releasing hormone receptor 2) (CRH-R 2) (CRF-RB)
DE (CRH-R2)
DE (CRH2 OR CRF2R)
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95224061; PubMed=7708757;
RA Perrin M., Donaldson C., Chen R., Blount A., Berggren T.,
RA Bilezikjian L., Sawchenko P., Vale W.;
RT Identification of a second corticotropin-releasing factor receptor
RT gene and characterization of a cDNA expressed in heart.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2969-2973(1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RX MEDLINE=95166778; PubMed=7755719;
RA Kishimoto T., Pearce R.V. II, Lin C.R., Rosenfeld M.G.;
RA "A sauvagine/corticotropin-releasing factor receptor expressed in
RT heart and skeletal muscle.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1108-1112(1995).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Heart;
RX MEDLINE=96015396; PubMed=7565810;
RA Stenzel P., Kesterson R., Yeung W., Cone R.D., Rittenberg M.B.,
RA Stenzel-Poore M.P.;
RT Identification of a novel murine receptor for
RT corticotropin-releasing hormone expressed in the heart.";
RL Mol. Endocrinol. 9:637-645(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
CC SHOWS HIGH-AFFINITY CRF BINDING. ALSO BINDS TO UROCORTIN I, II AND
CC III. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART. ALSO EXPRESSED
CC IN LUNGS, SKELETAL MUSCLE, GASTROINTESTINAL TRACT, EPIDIDYMIS, AND
CC BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC
CC EMBL; U17858; AAA68026.1; .
CC EMBL; U21729; AAC52174.1; .
CC EMBL; U19939; AAC52243.1; .
CC PIR; A56726; A56726.
CC PIR; I49149; I49149.
CC PIR; I49279; I49279.
CC MGD; MGI:894312; Crhr2.
CC GO; GO:0015056; F:corticotropin-releasing factor receptor ac. .; IDA.
CC GO; GO:0016525; P:negative regulation of angiogenesis, IMP.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; HormR; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 431
FT 2.
FT 138
FT DOMAIN 25 138
FT 1 (POTENTIAL).
FT TRANSSEM 139 159
FT 160 168
FT DOMAIN 169 188
FT 2 (POTENTIAL).
FT TRANSSEM 189 205
FT 206 229
FT TRANSSEM 230 243
FT 244 265
FT TRANSSEM 266 284
FT 285 307
FT TRANSSEM 308 330
FT 331 350
FT TRANSSEM 351 365
FT 366 385
FT TRANSSEM 386 431
FT 52 52
FT CARBOHYD 61 61
FT CARBOHYD 94 94
FT CARBOHYD 106 106
FT CARBOHYD 114 114
FT 3 5
FT CONFLICT 126 126
FT CONFLICT 392 393
FT CONFLICT 396 397
FT CONFLICT 408 408
SQ SEQUENCE 431 AA; 49923 MW; AGD9EDE575DB8061 CRC64;
Query Match 1.5%; Score 8; DB 1; Length 431;
Best Local Similarity 100.0%; Pred.No.5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
| | | | |
Db 369 SFQGFVVS 376

RESULT 46
CRF1_HUMAN
ID - CRF1_HUMAN STANDARD; PRT; 444 AA.
AC P34998; Q13008; Q9UK64;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
DE (Corticotropin-releasing hormone receptor 1) (CRH-R 1).
GN CRHR1 OR CRHR OR CRFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=94022296; PubMed=7692441;
RA Chen R., Lewis K.A., Perrin M.H., Vale W.W.;
RT "Expression cloning of a human corticotropin-releasing-factor
RT receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94063063; PubMed=8243652;
RA Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,
RA le Fur G., Caput D., Ferrara P.;
RT "Primary structure and functional expression of mouse pituitary and
RT human brain corticotropin releasing factor receptors.";
RL FEBS Lett. 335:1-5(1993).

RN SEQUENCE FROM N.A.
 RA Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN SEQUENCE FROM N.A. (ISOFORM CRF-R3).
 RP TISSUE=Hippocampus;
 RX MEDLINE=95110332; PubMed=7811272;
 RA Ross P.C., Kostas C.M., Ramabhadran T.V.;
 RT "A variant of the human corticotropin-releasing factor (CRF)
 RT receptor: cloning, expression and pharmacology";
 RL Biochem. Biophys. Res. Commun. 205:1836-1842(1994).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM CRF-R4).
 RX MEDLINE=20065650; PubMed=10598591;
 RA Grammatopoulos D.K., Dai Y., Randeve H.S., Levine M.A., Karteris E.,
 RA Easton A.J., Hillhouse E.W.;
 RT "A novel spliced variant of the type 1 corticotropin-releasing hormone
 RT receptor with a deletion in the seventh transmembrane domain present
 RT in the human pregnant term myometrium and fetal membranes.";
 RL Mol. Endocrinol. 13:2189-2202(1999).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR CORTICOTROPIN RELEASING FACTOR.
 CC SHOWS HIGH-AFFINITY CRF BINDING. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=CRF-R1;
 CC IsoId=P34998-1; Sequence=Displayed;
 CC Note=Major isoform;
 CC Name=CRF-R2;
 CC IsoId=P34998-2; Sequence=VSP_001997;
 CC Name=CRF-R3;
 CC IsoId=P34998-3; Sequence=VSP_001996, VSP_001997;
 CC Note=Does not bind to CRF with high affinity;
 CC Name=CRF-R4; Synonyms=ID;
 CC IsoId=P34998-4; Sequence=VSP_001997, VSP_001998;
 CC TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE CEREBELLUM,
 CC PITUITARY, CEREBRAL CORTEX AND OLFACTORY LOBE.
 CC -!- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; L23333; AAA35719.1; -;
 DR EMBL; L23332; AAA35718.1; -;
 DR EMBL; X72304; CAA51052.1; -;
 DR EMBL; AF039523; AAC69993.1; JOINED.
 DR EMBL; AF039510; AAC69993.1; JOINED.
 DR EMBL; AF039511; AAC69993.1; JOINED.
 DR EMBL; AF039512; AAC69993.1; JOINED.
 DR EMBL; AF039513; AAC69993.1; JOINED.
 DR EMBL; AF039514; AAC69993.1; JOINED.
 DR EMBL; AF039515; AAC69993.1; JOINED.
 DR EMBL; AF039516; AAC69993.1; JOINED.
 DR EMBL; AF039517; AAC69993.1; JOINED.
 DR EMBL; AF039518; AAC69993.1; JOINED.
 DR EMBL; AF039519; AAC69993.1; JOINED.
 DR EMBL; AF039520; AAC69993.1; JOINED.
 DR EMBL; AF039521; AAC69993.1; JOINED.
 DR EMBL; AF039522; AAC69993.1; JOINED.
 DR EMBL; U16273; AAC50073.1; -;
 DR EMBL; AF180301; AAD52688.1; -;
 DR PIR; I38879; I38879.
 DR PIR; I60975; A48260.
 DR Genew; HGNC:2357; CHR11.
 DR MIM; 122561; -.

DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0015056; F: corticotropin-releasing factor receptor ac. .; TAS.
 DR GO; GO:0007130; P: adenylate cyclase activation; TAS.
 DR GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleo. .; TAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR GO; GO:0007567; P: parturition; TAS.
 DR InterPro; IPR000832; GPCR_receptor.
 DR InterPro; IPR01879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G-PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G-PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS0227; G-PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G-PROTEIN_RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW phosphorylation; Alternative splicing.
 FT SIGNAL 1 23
 FT CHAIN 24 444
 FT CORTICOTROPIN RELEASING FACTOR RECEPTOR
 FT
 FT DOMAIN 24 121
 FT TRANSMEM 122 142
 FT DOMAIN 143 180
 FT TRANSMEM 181 200
 FT DOMAIN 201 218
 FT TRANSMEM 219 242
 FT DOMAIN 243 256
 FT TRANSMEM 257 278
 FT DOMAIN 279 297
 FT TRANSMEM 298 320
 FT DOMAIN 321 343
 FT TRANSMEM 344 363
 FT DOMAIN 364 378
 FT TRANSMEM 379 398
 FT DOMAIN 399 444
 FT DISULFID 30 54
 FT DISULFID 44 87
 FT DISULFID 68 102
 FT CARBOHYD 38 38
 FT CARBOHYD 45 45
 FT CARBOHYD 78 78
 FT CARBOHYD 90 90
 FT CARBOHYD 98 98
 FT VARSPLIC 41 81
 FT
 FT VARSPLIC 146 174
 FT
 FT VARSPLIC 385 398
 FT
 SQ SEQUENCE 444 AA; 50719 MW; 7221AEFF50E7AA8ED CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 SFQGFVVS 410
 Db 382 SFQGFVVS 389
 RESULT 47
 FCY2 YEAST
 ID FCY2_YEAST STANDARD; PRT; 533 AA.
 AC P17064;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 GN Purine-cytosine permease (PCP) (Cytosine/purine transport protein).
 GN FCY2 OR YER056C.
 OS Saccharomyces cerevisiae (Baker's yeast).

Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 VGYISIF 156
|||
Db 153 VGYISIF 159

Search completed: December 9, 2003, 09:01:13
Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2003, 08:57:00 : Search time 40 seconds
(without alignments)
3490.161 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 541
Sequence: 1 MAMLGASLHWGMLGSL.....DDILMEYSPRMSNPPTG 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_arChaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	621	4 Q8N429	Q8N429 homo sapien
2	38	7.0	169	11 Q9R1D4	Q9R1D4 mus musculus
3	38	7.0	237	11 Q8BUM8	Q8BUM8 mus musculus
4	38	7.0	546	11 Q91V95	Q91V95 mus musculus
5	27	5.0	575	13 Q9PWB7	Q9PWB7 brachydanio
6	20	3.7	94	13 Q9PRG1	Q9PRG1 ictalurus p
7	19	3.5	528	4 Q81V17	Q81V17 homo sapien
8	18	3.3	333	4 Q8N5V1	Q8N5V1 homo sapien
9	18	3.3	536	13 Q9PVD3	Q9PVD3 brachydanio
10	18	3.3	591	11 Q91WV4	Q91WV4 mus musculus
11	18	3.3	595	6 Q9TU31	Q9TU31 canis famil
12	18	3.3	964	4 Q8NHB4	Q8NHB4 homo sapien
13	16	3.0	419	13 Q8AXV3	Q8AXV3 fugu rubrip
14	13	2.4	418	13 Q91BG2	Q91BG2 gallus gall
15	13	2.4	444	13 Q9YHC6	Q9YHC6 rana ridibu
16	13	2.4	459	11 Q9J140	Q9J140 mus musculus

17	11	2.0	542	13 Q9PVD2	Q9PVD2 brachydanio
18	10	1.8	48	11 Q9J1Y4	Q9J1Y4 mus musculus
19	10	1.8	167	13 Q9YHC8	Q9YHC8 rana ridibu
20	10	1.8	227	4 Q8WUR8	Q8WUR8 homo sapien
21	9	1.7	91	13 Q98TU4	Q98TU4 brachydanio
22	9	1.7	202	13 Q98955	Q98955 meleagris g
23	9	1.7	374	6 Q8WME0	Q8WME0 ovis aries
24	9	1.7	402	6 Q8WQ99	Q8WQ99 ovis aries
25	9	1.7	419	13 Q8AXV4	Q8AXV4 fugu rubrip
26	9	1.7	459	11 Q8BGA4	Q8BGA4 mus musculus
27	9	1.7	465	13 Q73769	Q73769 carassius a
28	9	1.7	485	11 Q8KOB5	Q8KOB5 mus musculus
29	9	1.7	496	11 Q8BLT3	Q8BLT3 mus musculus
30	9	1.7	589	6 Q9GMD1	Q9GMD1 oryctolagus
31	8	1.5	37	4 Q8WXR5	Q8WXR5 homo sapien
32	8	1.5	126	13 Q57671	Q57671 meleagris g
33	8	1.5	168	13 Q9YHC7	Q9YHC7 rana ridibu
34	8	1.5	304	11 Q8BM22	Q8BM22 mus musculus
35	8	1.5	379	2 Q8RM00	Q8RM00 acinetobact
36	8	1.5	405	13 Q98UC1	Q98UC1 ameiturus ne
37	8	1.5	410	6 Q8WML9	Q8WML9 tupaia bela
38	8	1.5	414	13 Q8AWA1	Q8AWA1 oncorhynch
39	8	1.5	415	6 Q9BGU4	Q9BGU4 bos taurus
40	8	1.5	415	6 Q8WMM0	Q8WMM0 tupaia bela
41	8	1.5	415	11 Q8K3R2	Q8K3R2 mesocricetu
42	8	1.5	428	13 Q98UC0	Q98UC0 ameiturus ne
43	8	1.5	430	13 Q8AWA2	Q8AWA2 oncorhynch
44	8	1.5	437	6 Q8WML8	Q8WML8 tupaia bela
45	8	1.5	438	13 Q73768	Q73768 carassius a

ALIGNMENTS

RESULT 1

Q8N429 ID Q8N429 PRELIMINARY; PRT; 621 AA.

AC Q8N429, 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Parathyroid hormone receptor 2 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RP TISSUE=Brain;

RA Strausberg R.;

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC036811; AAH36811.1; -

DR InterPro; IPR000832; GPCR secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7cm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SMO0008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.

DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.

DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.

FT NON TER 1 1

SQ SEQUENCE 621 AA; 69299 MW; 8B0A5A84889436D2 CRC64;

Query Match 67.1%; Score 363; DB 4; Length 621;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 LGASLHWGMLGSLARALQSDGTITIEQIVLVKAKVOCENITIAQLQEGGNC 63
Db 75 LGASLHWGMLGSLARALQSDGTITIEQIVLVKAKVOCENITIAQLQEGGNC 134

```
QY 64 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDPMHSLNKTWYNS 123
Db 135 FPEWDLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDPMHSLNKTWYNS 194
QY 124 DCLRFLOPDISIGKQEFCEBRLYVMYTVGYSISFGSLAVAILIIGFRRLHCTRNVIHML 183
Db 195 DCLRFLOPDISIGKQEFCEBRLYVMYTVGYSISFGSLAVAILIIGFRRLHCTRNVIHML 254
QY 184 FVSEMLRATSIIVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSOYIGCKIAYVMF 243
Db 255 FVSEMLRATSIIVKDRVVHAHIGVKELESIMQDDPQNSIEATSDVKSOYIGCKIAYVMF 314
QY 244 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPFAAFVAAMAVARATLAD 303
Db 315 IYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFIILGWGFPFAAFVAAMAVARATLAD 374
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFINTVRLATKIWETNAVGHDTKQYRKLA 363
Db 375 ARCWELSGADIKWIYQAPILAAIGLNFILFINTVRLATKIWETNAVGHDTKQYRKLA 434
QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWBIIRHMCBLFNSFGFFVSIYCYCNGEVOAE 423
Db 435 STLVLVLVFGVHYIYFVCLPHSFTGLGWBIIRHMCBLFNSFGFFVSIYCYCNGEVOAE 494
QY 424 VKKMSRNWLSYDMKRTTPCGSRRCGSLVLTTHSTSSQSOVAA 467
Db 495 VKKMSRNWLSYDMKRTTPCGSRRCGSLVLTTHSTSSQSOVAA 538

RESULT 2
Q9R1D4
ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Parathyroid hormone type-2 receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC TISSUE=Brain;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Heilman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132083; AAD51909.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEPTOR_F2_4; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFINTVRLATKIWETNAVGH 353
Db 66 WIYQAPILAAIGLNFILFINTVRLATKIWETNAVGH 103

RESULT 3
Q8BUM8
ID Q8BUM8 PRELIMINARY; PRT; 237 AA.
AC Q8BUM8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; -.
DR EMBL; AF332077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
```

```
ID Q8BUM8 PRELIMINARY; PRT; 237 AA.
AC Q8BUM8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; -.
DR EMBL; AF332077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.

Query Match 7.0%; Score 38; DB 11; Length 237;
Best Local Similarity 100.0%; Pred. No. 3.9e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFINTVRLATKIWETNAVGH 353
Db 4 WIYQAPILAAIGLNFILFINTVRLATKIWETNAVGH 41

RESULT 4
Q91V95
ID Q91V95 PRELIMINARY; PRT; 546 AA.
AC Q91V95;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-Throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; -.
DR EMBL; AF332077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
```

```
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 546 AA; 61908 MW; 628051EF181A1DF3 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-31; Length 546;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 WIYQAPILAAIGLNFILNTVRVLATKIWETNAVGH 353
Db 313 WIYQAPILAAIGLNFILNTVRVLATKIWETNAVGH 350

RESULT 5
Q9PWB7
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone type-2 receptor.
GN PTHR2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RT J. Biol. Chem. 274:23035-23042(1999).
[2]
RN SEQUENCE FROM N.A.
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132081; AAD51907.1; -.
DR EMBL; AF132078; AAD51906.1; -.
DR EMBL; AF132079; AAD51906.1; JOINED.
DR EMBL; AF132080; AAD51906.1; JOINED.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 94 94
SQ SEQUENCE 94 AA; 10729 MW; D949182E1D2613EF CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-12; Length 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 FIYPLATNYWILVEGLYLH 262
Db 10 FIYPLATNYWILVEGLYLH 29

RESULT 7
Q8IV17
ID Q8IV17 PRELIMINARY; PRT; 528 AA.
AC Q8IV17;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to secretin receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035757; AAH35757.1; -.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 528 AA; 58944 MW; 6AFEE299E1A76BC2 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.7e-11; Length 528;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNVIHMLFVSF 187
Db 255 FRLHCTRNVIHMLFVSF 273

RESULT 8
Q8NSV1
ID Q8NSV1 PRELIMINARY; PRT; 333 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```



```
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DI Similar to parathyroid hormone receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031578; AAH31578.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 37588 MW; B176DBA5C6A68E4 CRC64;

Query Match 3.3%; Score 18; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYILVEGLYLH 262
DB 290 YFLATNYWYILVEGLYLH 307

RESULT 9
QPVND3
ID Q9PVD3 PRELIMINARY; PRT; 536 AA.
AC Q9PVD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone receptor PTHr.
GN PTHr.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-
RT related peptide receptor (PTHr) and a novel receptor (PTHrR) that is
RT preferentially activated by mammalian and fuguish parathyroid
RT hormone-related peptide.";
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132084; AAF01265.1; -.
DR HSSP; 003431; 1BL1.
DR ZFIN; ZDB-GENE-991123-8; pthrl.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DE2C8FA9 CRC64;
```

```
Query Match 3.3%; Score 18; DB 13; Length 536;
Best Local Similarity 100.0%; Pred. No. 9.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYNIHMLF 184
DB 167 GYFRLHCTRYNIHMLF 184

RESULT 10
Q91WV4
ID Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -.
DR MGD; MGI:97801; Pthr.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63B5BAFED CRC64;

Query Match 3.3%; Score 18; DB 11; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYILVEGLYLH 262
DB 290 YFLATNYWYILVEGLYLH 307

RESULT 11
Q9TU31
ID Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Parathyroid hormone receptor-1.
GN PTH1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RT "Molecular cloning and functional characterization of the canine
RT parathyroid hormone receptor-1 (PTH1).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSSP; Q03431; 1BL1.
```

DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 3.3%; Score 18; DB 6; Length 595;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 DB 289 YFLATNYWILVEGLYLH 306

RESULT 12

Q8NHB4 ID Q8NHB4 PRELIMINARY; PRT; 964 AA.
 AC Q8NHB4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsuchimi S., Aburatani H., Asai K., Akiyama Y.;
 RA "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB05462; BAC05721.1; -
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 3.
 DR Pfam; PF02793; HRM; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 964 AA; 105706 MW; 8EA72B44244DFD5D CRC64;

Query Match 3.3%; Score 18; DB 4; Length 964;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 |||||
 DB 564 YFLATNYWILVEGLYLH 581

RESULT 13

Q8AXV3 ID Q8AXV3 PRELIMINARY; PRT; 419 AA.
 AC Q8AXV3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vasoactive intestinal peptide receptor 1 A.
 GN VIPR1A.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontioidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
 RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
 RT in Fugu rubripes";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ296144; CAC82588.1; -
 KW Receptor.
 SQ SEQUENCE 419 AA; 47607 MW; F21C006AA4E1B698 CRC64;

Query Match 3.0%; Score 16; DB 13; Length 419;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNTHMLFVSF 187
 |||||
 DB 130 LHCTRNTHMLFVSF 145

RESULT 14

Q9IBG2 ID Q9IBG2 PRELIMINARY; PRT; 418 AA.
 AC Q9IBG2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Vasoactive intestinal peptide receptor (Fragment).
 GN CVIPR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21218647; PubMed=11319166;
 RA Kansaku N., Shimada K., Ohkubo T., Saito N., Suzuki T., Matsuda Y.,
 RA Zadworny D.;
 RT "Molecular cloning of chicken vasoactive intestinal polypeptide
 RT receptor complementary DNA, tissue distribution and chromosomal
 RT localization";
 RL Biol. Reprod. 64:1575-1581(2001).
 DR EMBL; AB029895; BAX95164.1; -
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 FT NON TER
 SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADC08FF3 CRC64;

Query Match 2.4%; Score 13; DB 13; Length 418;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNTHMLF 184
 |||||
 DB 130 LHCTRNTHMLF 142

RESULT 15

Q9YHC6 ID Q9YHC6 PRELIMINARY; PRT; 444 AA.
 AC Q9YHC6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)

AC Q9YIV4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Glucagon-like peptide 2 receptor (Fragment).
 GN GLP2R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWR/J; TISSUE=Small intestine;
 RA Bierknes M.; Cheng H.;
 RT "Clonal analysis of the effects of glucagon-like peptide 2 (GLP-2) and
 RT keratinocyte growth factor (KGF) on mouse intestinal epithelial
 RT progenitors."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF166265; AAF89584.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 48 48
 SQ SEQUENCE 48 AA; 5811 MW; 5D5B18AAEB3AF4AF CRC64;
 Query Match 1.8%; Score 10; DB 11; Length 48;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHM 181
 |||||
 Db 8 LHCTRYIHM 17

RESULT 19
 Q9YHC8 PRELIMINARY; PRT; 167 AA.
 AC Q9YHC8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glucagon receptor (Fragment).
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D.; Anouar Y.; Jegou S.; Fournier A.; Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 RT cyclase-activating polypeptide receptor exhibits pharmacological and
 RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 RT in mammals."
 RL Endocrinology 140:1285-1293(1999).
 DR EMBL; AF100642; AAD03600.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 167 167
 SQ SEQUENCE 167 AA; 19505 MW; 07AF68131034F517 CRC64;
 Query Match 1.8%; Score 10; DB 13; Length 167;
 Best Local Similarity 100.0%; Pred. No. 0.095;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264

Db 3 LVEGLYLHNL 12
 |||||
 RESULT 20
 Q8WUR8 PRELIMINARY; PRT; 227 AA.
 ID Q8WUR8;
 AC Q8WUR8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019818; AAH19818.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Hypothetical protein.
 FT NON_TER 1 1
 FT NON_TER 227 227
 SQ SEQUENCE 227 AA; 26334 MW; 2D24AEB3EABEC9E5 CRC64;
 Query Match 1.8%; Score 10; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRYIHM 181
 |||||
 Db 58 LHCTRYIHM 67

RESULT 21
 Q98TU4 PRELIMINARY; PRT; 91 AA.
 ID Q98TU4;
 AC Q98TU4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Pituitary adenylate cyclase-activating peptide (fragment).
 GN PACAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Wang Y.; Ge W.;
 RT "Cloning of zebrafish ovarian pituitary adenylate cyclase-activating
 RT peptide (PACAP) and regulation of its expression in the ovary."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF329633; AAK08503.1; -;
 DR ZFIN; ZDB-GENE-010406-4; pacap.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 FT NON_TER 1 1
 FT NON_TER 91 91
 SQ SEQUENCE 91 AA; 10240 MW; 8C9F32D8AD929BC CRC64;
 Query Match 1.7%; Score 9; DB 13; Length 91;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 172 LHCTRNTH 180
Db 80 LHCTRNTH 88

RESULT 22
Q98955
ID Q98955 PRELIMINARY; PRT; 202 AA.
AC Q98955; P87382;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-JAN-1999 (TRENBLrel. 09, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Glucagon receptor.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu C., You S., El Halawani M.E., Foster D.N.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U43446; AAB49831.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 202 AA; 23296 MW; B545A5F73888FAA8 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNTH 180
Db 19 LHCTRNTH 27

RESULT 23
Q98960
ID Q98960 PRELIMINARY; PRT; 374 AA.
AC Q98960;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson S.T., Kusters D.H.L., Barclay J.L., Pow D.V., Curlewis J.D.;
RT "Pituitary adenylate cyclase-activating polypeptide type 1 receptor
RT (PACIR) in the ewe hypothalamus: Implications for the control of
RT prolactin secretion.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY069986; AAL57759.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 374 AA; 43393 MW; 1192B6B2BAC575AD CRC64;

Query Match 1.7%; Score 9; DB 13; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNTH 180
Db 19 LHCTRNTH 27

RESULT 23
Q98960
ID Q98960 PRELIMINARY; PRT; 374 AA.
AC Q98960;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson S.T., Kusters D.H.L., Barclay J.L., Pow D.V., Curlewis J.D.;
RT "Pituitary adenylate cyclase-activating polypeptide type 1 receptor
RT (PACIR) in the ewe hypothalamus: Implications for the control of
RT prolactin secretion.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY069986; AAL57759.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 374 AA; 43393 MW; 1192B6B2BAC575AD CRC64;

Query Match 1.7%; Score 9; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSFMLRA 191
Db 172 LFVSFMLRA 180

RESULT 24
Q98969
ID Q98969 PRELIMINARY; PRT; 402 AA.
AC Q98969;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Pituitary adenylate cyclase-activating polypeptide type 1 receptor hop
DE 1 splice variant (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Anderson S.T., Kusters D.H.L., Barclay J.L., Pow D.V., Curlewis J.D.;
RT "Pituitary adenylate cyclase-activating polypeptide type 1 receptor
RT (PACIR) in the ewe hypothalamus: Implications for the control of
RT prolactin secretion.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY069987; AAL57760.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON_TER 402 402
SQ SEQUENCE 402 AA; 46611 MW; 682A384C8FC657DE CRC64;

Query Match 1.7%; Score 9; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSFMLRA 191
Db 172 LFVSFMLRA 180

RESULT 25
Q98974
ID Q98974 PRELIMINARY; PRT; 419 AA.
AC Q98974;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Vasoactive intestinal peptide receptor.
GN VIPR1B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
RT "Isolation and characterisation of the VIPR/PACAP receptor gene family
RT in Fugu rubripes.";

```

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ296143; CAC82597.1; -.

KW Receptor.

SQ SEQUENCE 419 AA; 47662 MW; 0B7A764B53BA2A7E CRC64;

Query Match 1.7%; Score 9; DB 13; Length 419;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIH 180

Db 133 LHCTRNVIH 141

RESULT 26

Q8BGA4

ID Q8BGA4 PRELIMINARY; PRT; 459 AA.

AC Q8BGA4;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type I receptor

DE precursor (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RE MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK047304; BAC33020.1; -.

DR EMBL; AK081121; BAC38140.1; -.

FT NON_TER

SQ SEQUENCE 459 AA; 52407 MW; B0B49556988E96DA CRC64;

Query Match

Best Local Similarity 1.7%; Score 9; DB 11; Length 459;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSFMLRA 191

Db 183 LFVSFMLRA 191

RESULT 27

O73769

ID O73769 PRELIMINARY; PRT; 465 AA.

AC O73769;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type 1

DE receptor.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

OX NCBI_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RA Wong A.O.B., Leung M.Y., Shea W.L.C., Chang J.P., Chow B.K.C.;

RT "Hypophysiotropic action of pituitary adenylate cyclase activating

RT polypeptide (PACAP) in the goldfish: immunohistochemical demonstration

RT of PACAP in the pituitary. PACAP stimulation of growth hormone release

RT from pituitary cells, and molecular cloning of pituitary type 1 PACAP

RT receptor.";

RT submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF048820; AAC15699.1; -.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.

DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.

DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

DR Receptor.

KW Receptor.

SQ SEQUENCE 465 AA; 53459 MW; 9779A95EDBFD1DC1 CRC64;

Query Match

Best Local Similarity 1.7%; Score 9; DB 13; Length 465;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 LFVSFMLRA 191

Db 184 LFVSFMLRA 192

RESULT 28

Q8K0B5

ID Q8K0B5 PRELIMINARY; PRT; 485 AA.

AC Q8K0B5;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Glucagon receptor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC Tissue=Liver;

RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC031885; AAH31885.1; -.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm_2; 1.

DR Pfam; PF02793; HRM; 1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.

DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.

DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.

DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

DR Receptor.

KW Receptor.

SQ SEQUENCE 485 AA; 54929 MW; 578EB30BF281E67A CRC64;

Query Match

Best Local Similarity 1.7%; Score 9; DB 11; Length 485;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIH 180

Db 170 LHCTRNVIH 178

RESULT 29

Q8BLT3

ID Q8BLT3 PRELIMINARY; PRT; 496 AA.

AC Q8BLT3;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Pituitary adenylate cyclase activating polypeptide type I receptor

DE precursor.

OS Mus musculus (Mouse).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSJBL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=1246851;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK042820; BAC31372.1; -.
SQ SEQUENCE 496 AA; 56649 MW; D6C6446F1E086939 CRC64;

Query Match 1.7%; Score 9; DB 11; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 LFVSPMLRA 191
Db 192 LFVSPMLRA 200
|||||

RESULT 30
Q9GMD1 PRELIMINARY; PRT; 589 AA.
AC Q9GMD1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PTH/PTHRP type I receptor.
OS PTHR.
GN Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA McCaughern-Carucci J.F., Mitnick M., Emanuel J.R., Dworetzky S.I.;
RT "Cloning and expression of the rabbit Type I PTH/PTHRP Receptor.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288463; AAG09046.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRN; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 589 AA; 64017 MW; 5FDF5DF8B61E72BB CRC64;

Query Match 1.7%; Score 9; DB 6; Length 589;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 YIYDFNHKG 97
Db 134 YIYDFNHKG 142
|||||

RESULT 31
Q8WXR5 PRELIMINARY; PRT; 37 AA.
AC Q8WXR5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
```

```
DE Corticotropin releasing hormone receptor variant 1g (Fragment).
GN CRHR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pisarchik A., Slominski A.T.;
RT "Alternative splicing of CRH-R1 receptors in human and mouse skin:
RT identification of new variants and their differential expression.";
RL FASEB J. 0:0-0 (2001).
DR EMBL; AF389653; AAL46633.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4488 MW; AE2A8DCD18B35517 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
Db 14 SFQGFVVS 21
|||||

RESULT 32
OS7671 PRELIMINARY; PRT; 126 AA.
AC OS7671;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Parathyroid hormone receptor (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu C., You S., El Halawani M.E., Foster D.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94326; AAG93893.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLH 262
Db 6 LVEGLYLH 13
|||||

RESULT 33
Q9YHC7 PRELIMINARY; PRT; 168 AA.
AC Q9YHC7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Secretin receptor (Fragment).
```

```

OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]_TaxID=8406;
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99165178; PubMed=10067855;
RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
RT cyclase-activating polypeptide receptor exhibits pharmacological and
RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
RT in mammals.";
RL Endocrinology 140:1285-1293(1999).
DR EMBL; AF100643; AA03601.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm 2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 19610 MW; 2EDD1A4B16916FB2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 168;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLH 262
Db 3 LVEGLYLH 10

RESULT 34
Q8BM22 PRELIMINARY; PRT; 304 AA.
AC Q8BM22;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to glucagon-like peptide 2 receptor precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK035702; BAC29159.1; -.
SQ SEQUENCE 304 AA; 34448 MW; B668FDA12EB9FD4D CRC64;

Query Match 1.5%; Score 8; DB 11; Length 304;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLH 262
Db 72 LVEGLYLH 79

RESULT 35
Q8RM00 PRELIMINARY; PRT; 379 AA.
AC Q8RM00;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

```

```

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Acyl coenzyme A dehydrogenase.
GN HCAD.
OS Acinetobacter sp. ADP1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]_TaxID=62977;
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=90130333; PubMed=2298704;
RA Hartnett C., Neidle E.L., Ngai K.L., Ornston L.N.;
RT "DNA sequences of genes encoding Acinetobacter calcoaceticus
RT protocatechuate 3,4-dioxygenase: evidence indicating shuffling of
RT genes and of DNA sequences within genes during their evolutionary
RT divergence.";
RL J. Bacteriol. 172:956-966(1990).
RN [2]_TaxID=956-966(1990).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=93194074; PubMed=8449410;
RA DiMarco A.A., Averhoff B.A., Kim E.E., Ornston L.N.;
RT "Evolutionary divergence of pobaA, the structural gene encoding p-
RT hydroxybenzoate hydroxylase in an Acinetobacter calcoaceticus strain
RT well-suited for genetic analysis.";
RL Gene 125:25-33(1993).
RN [3]_TaxID=25-33(1993).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=93232329; PubMed=8331077;
RA DiMarco A.A., Averhoff B., Ornston L.N.;
RT "Identification of the transcriptional activator pobaR and
RT characterization of its role in the expression of pobaA, the structural
RT gene for p-hydroxybenzoate hydroxylase in Acinetobacter
RT calcoaceticus.";
RL J. Bacteriol. 175:4499-4506(1993).
RN [4]_TaxID=4499-4506(1993).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=94237485; PubMed=8181753;
RA Hartnett G.B., Ornston L.N.;
RT "Acquisition of apparent DNA slippage structures during extensive
RT evolutionary divergence of pbad and catD genes encoding identical
RT catalytic activities in Acinetobacter calcoaceticus.";
RL Gene 142:23-29(1994).
RN [5]_TaxID=23-29(1994).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=94341565; PubMed=8063101;
RA Kowalchuk G.A., Hartnett G.B., Benson A., Houghton J.E., Ngai K.L.,
RA Ornston L.N.;
RT "Contrasting patterns of evolutionary divergence within the
RT Acinetobacter calcoaceticus pca operon.";
RL Gene 146:23-30(1994).
RN [6]_TaxID=23-30(1994).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=95095936; PubMed=8002591;
RA Elsemore D.A., Ornston L.N.;
RT "The pca-pob supraparallel cluster of Acinetobacter calcoaceticus
RT contains quiaA, the structural gene for quinate-shikimate
RT dehydrogenase.";
RL J. Bacteriol. 176:7659-7666(1994).
RN [7]_TaxID=7659-7666(1994).
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=98175676; PubMed=9515921;
RA Gerischer U., Segura A., Ornston L.N.;
RT "PcaU, a transcriptional activator of genes for protocatechuate
RT utilization in Acinetobacter.";
RL J. Bacteriol. 180:1512-1524(1998).
RN [8]_TaxID=1512-1524(1998).
RP SEQUENCE FROM N.A.

```



```

RC STRAIN=ADP1;
RA Smith M.A., Young D.M., Ornston L.N.;
RT "Genetic analysis of the metabolism of phenylpropanoid compounds in
RL Acinetobacter strain ADP1.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; L05770; AAL54851.1; -.
DR InterPro; IPR006089; Acyl-CoA dh.
DR InterPro; IPR006090; Acyl-CoA dh C.
DR InterPro; IPR006091; Acyl-CoA dh M.
DR InterPro; IPR006092; Acyl-CoA dh N.
DR Pfam; PF00441; Acyl-CoA dh_1.
DR Pfam; PF02770; Acyl-CoA dh_M; 1.
DR Pfam; PF02771; Acyl-CoA dh_N; 1.
DR PROSITE; PS00072; ACYL COA DH 1; 1.
DR PROSITE; PS00073; ACYL COA DH 2; 1.
SQ SEQUENCE 379 AA; 42182 MW; 085705F2EDD70DE3 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 FGS LAVAI 163
DB 79 FGS LAVAI 86

RESULT 36
Q98UC1 PRELIMINARY; PRT; 405 AA.
AC Q98UC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Corticotropin releasing factor receptor 2.
OS Aneurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ameiurus.
OX NCBI_TaxID=27778;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066341; PubMed=11145609;
RA Arai M., Assil I.Q., Abou-Samra A.B.;
RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
RT Catfish: A Novel Third Receptor Is Predominantly Expressed in
RT Pituitary and Urophysis.";
RL Endocrinology 142:446-454(2001).
DR EMBL; AF229360; AAK01089.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hoimr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 405 AA; 46823 MW; E05E96BCFEAD5CC5 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 405;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
DB 343 SFQGFVVS 350

RESULT 37
Q8WML9 PRELIMINARY; PRT; 410 AA.
ID Q8WML9
AC Q8WML9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 2.
GN CRPR2.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277158; CAC81754.1; -.
DR Receptor.
KW Receptor.
SQ SEQUENCE 414 AA; 48329 MW; 11FB2E9E481CCC2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 414;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Corticotropin releasing factor type 2A receptor.
GN CRF2A.
OS Tupiaia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RA Dautzenberg F.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99288234; PubMed=10336722;
RA Palchoudhuri M.R., Hauger R.L., Wille S., Fuchs E., Dautzenberg F.M.;
RT "Isolation and pharmacological characterization of two functional
RT splice variants of corticotropin-releasing factor type 2 receptor from
RT the tree shrew (Tupaia belangeri).";
RL J. Neuroendocrinol. 11:419-428(1999).
DR EMBL; AJ422424; CAD19578.1; -.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hoimr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 410 AA; 47613 MW; 09AB660341A63DDC CRC64;

Query Match 1.5%; Score 8; DB 6; Length 410;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVVS 410
DB 348 SFQGFVVS 355

RESULT 38
Q8AWA1 PRELIMINARY; PRT; 414 AA.
ID Q8AWA1
AC Q8AWA1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 2.
GN CRPR2.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277158; CAC81754.1; -.
DR Receptor.
KW Receptor.
SQ SEQUENCE 414 AA; 48329 MW; 11FB2E9E481CCC2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 414;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 403 SFQGFVS 410
DB 352 SFQGFVS 359

RESULT 39
Q9BGU4 PRELIMINARY; PRT; 415 AA.
AC Q9BGU4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
DE Corticotropin-releasing hormone receptor.
GN CRFR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RA Takata M., Sekikawa K.;
RT "Molecular Cloning of Bovine corticotropin-releasing hormone receptor
CDNA.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055434; BAB21864.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47754 MW; 4A54A3DCE6CF2319 CRC64;

Query Match 1.5%; Score 8; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
DB 353 SFQGFVS 360

RESULT 40
Q8WMM0 PRELIMINARY; PRT; 415 AA.
AC Q8WMM0;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Corticotropin releasing factor type 1 receptor.
GN CRF1.
OS Tupia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiidae;
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC Dautzenberg F.M.;
RA Dautzenberg F.M.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99067019; PubMed=9851694;
RA Paichaudhuri M.R., Wille S., Mevenkamp G., Spiess J., Fuchs E.,
RA Dautzenberg F.M.;
RT "Corticotropin-releasing factor receptor type 1 from Tupia belangeri:
cloning, functional expression and tissue distribution.";

```

```

RL Eur. J. Biochem. 258:78-84(1998).
DR EMBL; AJ422241; CAD19577.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47685 MW; 97BE9AEB050AC08D CRC64;

Query Match 1.5%; Score 8; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
DB 353 SFQGFVS 360

RESULT 41
Q8K3R2 PRELIMINARY; PRT; 415 AA.
AC Q8K3R2;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Type-1 corticotropin-releasing hormone receptor alpha isoform.
GN CRH-R1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Pisarchik A.V., Slominski A.;
RT "Hamster CRH receptor type 1 (alpha) mRNA coding sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034599; AAK59707.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
XW Receptor.
SQ SEQUENCE 415 AA; 47703 MW; 500B4DD617E5F19E CRC64;

Query Match 1.5%; Score 8; DB 11; Length 415;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SFQGFVS 410
DB 353 SFQGFVS 360

RESULT 42
Q98UC0 PRELIMINARY; PRT; 428 AA.
AC Q98UC0;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

```

```

DE Corticotropin releasing factor receptor 3.
OS Ameiurus nebulosus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ameiurus.
OX NCBI_TaxID=27778;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066341; PubMed=11145609;
RA Arai M., Assil I.Q., Abou-Samra A.B.;
RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
RT Catfish: A Novel Third Receptor Is Predominantly Expressed in
RT Pituitary and Urophysis.";
RL Endocrinology 142:446-454(2001).
DR EMBL; AF229361; AAK01070.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SMO0008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 428 AA; 49406 MW; 63F9C07AFEF5B27 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 428;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 366 SFQGFVVS 373

RESULT 43
Q8AWA2 PRELIMINARY; PRT; 430 AA.
AC Q8AWA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin-releasing factor receptor type 1.
GN CRPR1.
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Pohl S., Darlison M.G., Lederis K., Richter D.;
RT "Corticotropin-releasing factor receptors from teleost fish:
RT evolutionary conservation of sequence, functional expression and
RT second messenger coupling.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ27157; CAC81753.1; -.
KW Receptor.
SQ SEQUENCE 430 AA; 49595 MW; BCD2CDF36B1281A2 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 430;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 368 SFQGFVVS 375

RESULT 44

```

```

Q8WML8 PRELIMINARY; PRT; 437 AA.
AC Q8WML8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Corticotropin releasing factor type 2B receptor.
GN CRF2B.
OS Tupia belangeri (Northern tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99288234; PubMed=10336722;
RA Palchaudhuri M.R., Hauger R.L., Wille S., Fuchs E., Dautzenberg F.M.;
RT "Isolation and pharmacological characterization of two functional
RT splice variants of corticotropin-releasing factor type 2 receptor from
RT the tree shrew (Tupaia belangeri)".
RL J. Neuroendocrinol. 11:419-428(1999).
DR EMBL; AJ422443; CAD19579.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SMO0008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 437 AA; 50330 MW; E4721B7D880E1B07 CRC64;

Query Match 1.5%; Score 8; DB 6; Length 437;
Best Local Similarity 100.0%; Pred.No.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 SFQGFVVS 410
Db 375 SFQGFVVS 382

RESULT 45
O73768 PRELIMINARY; PRT; 438 AA.
AC O73768;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth-hormone releasing hormone-like peptide receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX Chan K.W., Yu K.L., Rivier J., Chow B.K.C.;
RT "Identification and characterization of a receptor from goldfish
RT specific for a teleost growth hormone-releasing hormone-like
RT peptide.";
RL Neuroendocrinology 0:0-0(1998).
DR EMBL; AF048819; AAC15698.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.

```

DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECF_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECF_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 438 AA; 50305 MW; C3516A52D692C339 CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 438;
 Best Local Similarity 100.0%; Pred.No.29; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 173 HCTENYIH 180
 |||||
 Db 165 HCTENYIH 172
 RESULT 46
 Q98UC2 PRELIMINARY; PRT; 445 AA.
 AC Q98UC2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Corticotropin releasing factor receptor 1.
 OS Ameiurus nebulosus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ameiurus.
 OC NCBI_TaxID=27778;
 [1]
 RN RNP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21066341; PubMed=11145609;
 RA Arai M., Assil I.Q., Abou-Samra A.B.;
 RT "Characterization of Three Corticotropin-Releasing Factor Receptors in
 Catfish: A Novel Third Receptor Is Predominantly Expressed in
 Pituitary and Urophysis";
 RL Endocrinology 142:446-454(2001).
 DR EMBL: AF229359; AA01068.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECF_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECF_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 445 AA; 51062 MW; F17DA70BE22BB755 CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 445;
 Best Local Similarity 100.0%; Pred.No.30; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 403 SFQGFVVS 410
 |||||
 Db 383 SFQGFVVS 390
 RESULT 47
 Q8NG71 PRELIMINARY; PRT; 447 AA.
 AC Q8NG71;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RN RNP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21148137; PubMed=11250547;
 RA Sivarajah P., Wheeler M.B., Irwin D.M.;
 RT "Evolution of receptors for proglucagon-derived peptides: isolation of
 frog glucagon receptors";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 128:517-527(2001).
 DR EMBL: AF318179; AAL37167.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECF_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECF_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 489 AA; 56746 MW; 39385EC76D68C84F CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 489;
 Best Local Similarity 100.0%; Pred.No.32; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 146 VMYTVGYS 153
 |||||
 Db 137 VMYTVGYS 144
 RESULT 49

RP SEQUENCE FROM N.A.
 RA Swa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Itutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB065967; BAC06179.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECF_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECF_F2_4; 1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 447 AA; 51070 MW; 6C4EDBDC5197FBCD CRC64;
 Query Match 1.5%; Score 8; DB 4; Length 447;
 Best Local Similarity 100.0%; Pred.No.30; Mismatches 8; Conservative 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 403 SFQGFVVS 410
 |||||
 Db 385 SFQGFVVS 392
 RESULT 48
 Q8UVY4 PRELIMINARY; PRT; 489 AA.
 AC Q8UVY4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glucagon receptor.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_TaxID=8404;
 [1]
 RN RNP
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21148137; PubMed=11250547;
 RA Sivarajah P., Wheeler M.B., Irwin D.M.;
 RT "Evolution of receptors for proglucagon-derived peptides: isolation of
 frog glucagon receptors";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 128:517-527(2001).
 DR EMBL: AF318179; AAL37167.1; -;
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormu_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECF_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECF_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 489 AA; 56746 MW; 39385EC76D68C84F CRC64;
 Query Match 1.5%; Score 8; DB 13; Length 489;
 Best Local Similarity 100.0%; Pred.No.32; Mismatches 8; Conservative 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 146 VMYTVGYS 153
 |||||
 Db 137 VMYTVGYS 144
 RESULT 49

Q8SZ04 PRELIMINARY; PRT; 580 AA.
 ID Q8SZ04
 AC Q8SZ04
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE REP25570P
 GN HEP OR CG2190 OR CG4353. (Fruit fly).
 OS Drosophila melanogaster
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY071210; AAL48832.1; -;
 DR FlyBase: FBgn010303; hep.
 SQ SEQUENCE 580 AA; 61880 MW; 3596898A7A7A5F9F CRC64;
 Query Match 1.5%; Score 8; DB 5; Length 580;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 456 THSTSSQS 463
 DB 239 THSTSSQS 246
 RESULT 50
 Q917S3 PRELIMINARY; PRT; 580 AA.
 ID Q917S3
 AC Q917S3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CG4353 protein.
 GN HEP OR CG2190 OR CG4353.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Adams M.D., Celniker S.E., PubMed=10731132;
 RA MEDLINE=20196006;
 RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Niklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glorid A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reine B.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003491; AAG22351.2; -;
 DR FlyBase: FBgn0010303; hep.
 SQ SEQUENCE 580 AA; 61938 MW; 9A968998AB57A5F9E CRC64;
 Query Match 1.5%; Score 8; DB 5; Length 580;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 456 THSTSSQS 463
 DB 239 THSTSSQS 246
 Search completed: December 9, 2003, 09:02:06
 Job time : 42 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:32:16 ; Search time 21 Seconds
(without alignments)
2477.488 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGASLHVWGLMLGSL.....DDILMEKSRPMESNPDTG 541

Scoring table: OLIGO
Gap 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1979

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	363	67.1	550	2 A57519	parathyroid hormon
2	25	4.6	585	2 A39286	parathyroid hormon
3	19	3.5	440	2 JC2532	secretin receptor
4	19	3.5	449	2 S16319	secretin receptor
5	18	3.3	589	2 I59297	parathyroid hormon
6	18	3.3	591	2 S44203	parathyroid hormon
7	18	3.3	593	2 I54195	parathyroid hormon
8	18	3.3	593	2 A49191	parathyroid hormon
9	13	2.4	455	2 I53273	gastric inhibitory
10	13	2.4	459	2 JH0594	vasoactive intesti
11	13	2.4	460	2 JC2194	vasoactive intesti
12	13	2.4	462	2 JC2462	gastric inhibitory
13	13	2.4	495	2 JC2195	vasoactive intesti
14	12	2.2	466	2 G02234	gastric inhibitory
15	12	2.2	466	2 S66776	glucose-dependent
16	12	2.2	491	2 I37411	glucose-dependent
17	10	1.8	477	2 JC2041	glucagon receptor
18	9	1.7	381	2 S33449	pituitary adenyilat
19	9	1.7	437	2 JU0185	PACAP/VIP receptor
20	9	1.7	437	2 S39069	vasoactive intesti
21	9	1.7	438	2 G02822	vasoactive intesti
22	9	1.7	463	2 S71624	glucagon-like pept
23	9	1.7	463	2 A46172	glucagon-like pept
24	9	1.7	463	2 I84494	glucagon-like pept
25	9	1.7	467	2 JN0616	pituitary adenyilat
26	9	1.7	485	2 JQ1957	glucagon receptor
27	9	1.7	485	2 JC4363	glucagon receptor
28	9	1.7	495	2 S36114	pituitary adenyilat
29	9	1.7	495	2 S39061	pituitary adenyilat

30	9	1.7	513	2 S47631	pituitary adenyilat
31	9	1.7	523	2 S39060	pituitary adenyilat
32	9	1.7	525	2 JN0902	pituitary adenyilat
33	8	1.5	375	2 I38879	corticotropin rele
34	8	1.5	411	2 A55610	corticotropin-rele
35	8	1.5	411	2 S26195	probable carboxyl-
36	8	1.5	415	2 S39535	corticotropin-rele
37	8	1.5	415	2 I58144	corticotropin-rele
38	8	1.5	430	2 A56726	corticoliberin rec
39	8	1.5	431	2 I49279	sauvagine/corticot
40	8	1.5	431	2 I49149	CRF receptor - mou
41	8	1.5	444	2 A48260	corticoliberin rec
42	8	1.5	533	1 GRBYCP	cytosine/purine tr
43	8	1.5	1904	2 T13256	tall-host specific
44	7	1.3	50	2 B37334	L-mandelate dehydr
45	7	1.3	80	2 AB2755	host factor I [imp

ALIGNMENTS

RESULT 1

A57519
parathyroid hormone receptor 2 precursor - human
N:Alternate names: PTH2 receptor
C:Species: ~~homo-sapiens~~ (man)
C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C:Accession: A57519
R:Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A:Title: Identification and functional expression of a receptor selectively recognizing
A:Reference number: A57519; MUID:95318121; PMID:7797535
A:Accession: A57519
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-550 <USD>
A:Cross-references: GB:U25128; NID:9887966; PIDN:AAC50157.1; PID:9887967
C:Genetics:
A:Gene: GDB: PTHR2; PTHR2R
A:Cross-references: GDB:731977; OMIM:601469
A:Map position: 2q33-2q33
C:Superfamily: glucagon receptor
C:Keywords: hormone receptor

Query Match	67.1%	Score	363;	DB	2;	Length	550;
Best Local Similarity	99.8%	Pred. No.	0;				
Matches	463;	Conservative	0;	Mismatches	1;	Indels	0;
				Gaps	0;		
QY	4	LGASLHVWGLMLGSCLLARAQLDSGGTTTIEQIVLVLKAKVQCELNITAOLOEGGNC	63				
Db	4	LGASLHVWGLMLGSCLLARAQLDSGGTTTIEQIVLVLKAKVQCELNITAOLOEGGNC	63				
QY	64	FPEWDLICWPRTGVGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFHSLNKTWANY	123				
Db	64	FPEWDLICWPRTGVGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFHSLNKTWANY	123				
QY	124	DCLRFLOPDISIGKQFCERLYVMYTVGYISIFGSLAVAIIIGYPRRLHCTRNYYHML	183				
Db	124	DCLRFLOPDISIGKQFCERLYVMYTVGYISIFGSLAVAIIIGYPRRLHCTRNYYHML	183				
QY	184	FVSFMLRATSFVKORVVAHIGVKELESIMQDDPQNSIEATSDVKSQYIGCKIAVVMF	243				
Db	184	FVSFMLRATSFVKORVVAHIGVKELESIMQDDPQNSIEATSDVKSQYIGCKIAVVMF	243				
QY	244	IYFLATNYWILVEGILYHNLIFVAFPSDKYLMGFILGWGFPFAAFVAARATLAD	303				
Db	244	IYFLATNYWILVEGILYHNLIFVAFPSDKYLMGFILGWGFPFAAFVAARATLAD	303				
QY	304	ARCWELSGADIKWIYQAPILAAIGLNFILNTRVRLATKIWETNAVGHDTKQYRKLAK	363				
Db	304	ARCWELSGADIKWIYQAPILAAIGLNFILNTRVRLATKIWETNAVGHDTKQYRKLAK	363				
QY	364	STLVLVLVFGVHYIVFVCLPHSFTGLGWIRMHCBELFFNSFOGFFVSIITYCYCNGEQAE	423				

Db 364 STLVLVFGVHYIYFVCLPHSFTHGLGWEIRHCELFNFSGQFFVSIYCYCNGEVOAE 423
QY 424 VKQWMSRWNLSDWKRTPPCGSRRCGSVLTVTWTHSTSSQSQA 467
Db 424 VKQWMSRWNLSDWKRTPPCGSRRCGSVLTVTWTHSTSSQSQA 467

RESULT 2
A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 11-Jan-2000
C:Accession: A39286
R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K
Science 254, 1024-1026, 1991
A:Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
A:Reference number: A39286; MUID:92054592; PMID:1658941
A:Accession: A39286
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-585 <JUE>
A:Cross-references: GB:M74445
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.5e-17; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNYYIHMLFVSFMLRA 191
Db 207 GYFRLHCTRNYYIHMLFVSFMLRA 231

RESULT 3
JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin rece
A:Reference number: JC2532; MUID:95169147; PMID:7864894
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JIA>
A:Cross-references: EMBL:U20178; NID:G662795; PIDN:AAC50106.1; PID:G662796
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:SCTR
A:Cross-references: GDB:270546; OMIM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor

Query Match 3.5%; Score 19; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 7e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYIHMLFVSF 187
Db 167 FRLHCTRNYYIHMLFVSF 185

RESULT 4
S16319
secretin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S16319
R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.

EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319; MUID:91266890; PMID:1646711
A:Accession: S16319
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: EMBL:X59132; NID:G57228; PIDN:CAA41849.1; PID:G57229
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 7.1e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYYIHMLFVSF 187
Db 167 FRLHCTRNYYIHMLFVSF 185

RESULT 5
159297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I59297
R:McQuaig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyr
A:Reference number: I59297; MUID:94255468; PMID:8197183
A:Accession: I59297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-589 <RES>
A:Cross-references: GB:I34611; NID:G530149; PIDN:AAA40011.1; PID:G530151
C:Genetics:
A:Gene: PTHR
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 9.4e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYTWILVEGLYLH 262
Db 290 YFLATNYYTWILVEGLYLH 307

RESULT 6
S44203
parathyroid hormone-related peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S44203
R:Karperien, M.; van Dijk, T.B.; Hoelmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boons
submitted to the EMBL Data Library, April 1994
A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related p
A:Reference number: S44203
A:Accession: S44203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-591 <KAR>
A:Cross-references: EMBL:X78936; NID:G474828; PIDN:CAA55536.1; PID:G474829
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 9.5e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYTWILVEGLYLH 262
Db 290 YFLATNYYTWILVEGLYLH 307

RESULT 7

I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C:Accession: I54195; A42698
R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A:Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor
and rat genomes.
A:Reference number: I54195; MUID:94292182; PMID:8020952
A:Accession: I54195
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-591 <RES>
A:Cross-references: GB:I19475; NID:g467316; PIDN:AAA68098.1; PID:g467317
R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A:Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol triphosphates and increases intracellular free calcium.
A:Reference number: A42698; MUID:92212903; PMID:1313566
A:Accession: A42698
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-585, 'G', 587-591 <ABO>
A:Experimental source: ROS 17/2.8 osteosarcoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:92187)
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 9.5e-10; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

Qy 245 YFLATNYWILVEGLYH 262
|||||
Db 290 YFLATNYWILVEGLYH 307

RESULT 8

A49191
parathyroid hormone/PTH-related peptide receptor - human
N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: I38139; A49191; I38113; G01562; S29610
R:Schipani, E.; Weinstein, I.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A:Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
A:Reference number: I38139; MUID:95263723; PMID:7745008
A:Accession: I38139
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-593 <RES>
A:Cross-references: EMBL:U22409; NID:g897594; PIDN:AAAB0657.1; PID:g897596
R:Schipani, E.; Karga, H.; Karaplis, A.C.; Fotts Jr., J.F.; Kronenberg, H.M.; Segre, G.V.
Endocrinology 132, 2157-2165, 1993
A:Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
A:Reference number: A49191; MUID:93238641; PMID:8386612
A:Accession: A49191
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-593 <SCH>
A:Cross-references: GB:I04308; NID:gl90721; PIDN:AAA36525.1; PID:gl90722
A:Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Morva, N.R.
Eur. J. Pharmacol. 246, 149-155, 1993
A:Title: Cloning and functional expression of a human parathyroid hormone receptor.
A:Reference number: I38113; MUID:93387403; PMID:8397094
A:Accession: I38113
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-593 <RE2>
A:Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R:Levine, M.
submitted to the EMBL Data Library, November 1994
A:Reference number: G07787
A:Accession: G01562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-593 <LEV>
A:Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130
C:Genetics:
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.3%; Score 18; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262
|||||
Db 290 YFLATNYWILVEGLYH 307

RESULT 9

I53273
gastric inhibitory polypeptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
C:Accession: I53273
R:Ussdin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.
Endocrinology 133, 2861-2870, 1993
A:Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive
A:Reference number: I53273; MUID:94062667; PMID:8243312
A:Accession: I53273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-455 <RES>
A:Cross-references: GB:I19660; NID:g431448; PIDN:AAAC37637.1; PID:g431449
C:Superfamily: glucagon receptor

Query Match 2.4%; Score 13; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNVIHM 181
|||||
Db 159 FRLHCTRNVIHM 171

RESULT 10

JH0594
vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: JH0594; S56014
R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A:Title: Functional expression and tissue distribution of a novel receptor for vasoact
A:Reference number: JH0594; MUID:92232309; PMID:1314625
A:Accession: JH0594
A:Molecule type: mRNA
A:Residues: 1-459 <ISH>
A:Cross-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A:Experimental source: lung
R:Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5
A:Reference number: S56014; MUID:97104266; PMID:8948424
A:Accession: S56014
A:Status: preliminary; translation not shown
A:Molecule type: DNA

A;Residues: 1-26 <PEI>
A;Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
|||||
Db 171 LHCTRNVIHMLF 183

RESULT 11
JC2194
vasoactive intestinal peptide receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 05-Nov-1999
C;Accession: JC2194; UN0604; F02289; S38397
R;Couvineau, A.; Rouyer-Pessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2194
A;Molecule type: mRNA
A;Residues: 1-460 <COU>
A;Cross-references: EMBL:X75299; NID:g407461; PIDN:CAAS3046.1; PID:g407462
A;Experimental source: jejunal epithelial cell; clone HIVR8
R;Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A;Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin
A;Reference number: UN0604; MUID:93290841; PMID:8390245
A;Accession: UN0604
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-284,288-460 <SRE>
A;Cross-references: GB:L13288; NID:g292903; PIDN:AA336805.1; PID:g292904
R;Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Pessard, C.; Nicole, P.; Laburthe, M.
Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A;Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A;Reference number: PC2289; MUID:95118345; PMID:7818527
A;Accession: PC2289
A;Molecule type: mRNA
A;Residues: 63-129 <CO2>
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVRI
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pr
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F;145-168/Domain: transmembrane #status predicted <TM1>
F;176-194/Domain: transmembrane #status predicted <TM2>
F;216-234/Domain: transmembrane #status predicted <TM3>
F;255-277/Domain: transmembrane #status predicted <TM4>
F;299-319/Domain: transmembrane #status predicted <TM5>
F;346-363/Domain: transmembrane #status predicted <TM6>
F;377-396/Domain: transmembrane #status predicted <TM7>
F;58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

F;450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
|||||
Db 170 LHCTRNVIHMLF 182

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N;Alternate names: GIP receptor
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2462
R;Iasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islet
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:g644880; PIDN:BAA07284.1; PID:g765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>

Query Match 2.4%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHM 181
|||||
Db 159 FRLHCTRNVIHM 171

RESULT 13
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone HIVR5) - huma
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C;Accession: JC2195; S42087
R;Couvineau, A.; Rouyer-Pessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Der
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA
A;Reference number: JC2194; MUID:94235025; PMID:8179610
A;Accession: JC2195
A;Molecule type: mRNA
A;Residues: 1-495 <COU>
A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAAS4814.1; PID:g456353
A;Experimental source: jejunal epithelial cell
C;Genetics:
A;Gene: GDB:VIPR1; RCD1; HVRI
A;Cross-references: GDB:128589; OMIM:192321
A;Map position: 3p22-3p22
C;Superfamily: glucagon receptor
C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status predi
F;180-203/Domain: transmembrane #status predicted <TM1>
F;211-229/Domain: transmembrane #status predicted <TM2>
F;251-269/Domain: transmembrane #status predicted <TM3>
F;290-312/Domain: transmembrane #status predicted <TM4>
F;334-354/Domain: transmembrane #status predicted <TM5>

F;381-398/Domain: transmembrane #status predicted <TM6>
F;412-431/Domain: transmembrane #status predicted <TM7>
F;93,104,135,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYHMLF 184
Db 205 LHCTRNYYHMLF 217
|||||

RESULT 14

G02234
gastric inhibitory polypeptide receptor - human
N;Alternate names: GIP receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C;Accession: G02234
R;Bonner, T.I.; Usdin, T.B.
submitted to the EMBL Data Library, October 1995
A;Reference number: G09336
A;Accession: G02234
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-466 <BON>
A;Cross-references: EMBL:U39231; NID:g1066050; PIDN:AAA4418.1; PID:g1066051
C;Genetics:
A;Gene: GDB:GIPR
A;Cross-references: GDB:335023
A;Map position: 19q13.3-19q13.3
C;Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRELHCTRNYYH 180
Db 162 FRELHCTRNYYH 173
|||||

RESULT 15

S66676
glucose-dependent insulinotropic protein receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S66676
R;Volz, A.; Goeke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
FEBS Lett. 373, 23-29, 1995
A;Title: Molecular cloning, functional expression, and signal transduction of the GIP-receptor
A;Reference number: S66676; MUID:96013879; PMID:7589426
A;Accession: S66676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <VOL>
A;Cross-references: GB:S79852
A;Note: the authors translated the codon GCC for residue 427 as Leu
C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRELHCTRNYYH 180
Db 162 FRELHCTRNYYH 173
|||||

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:28:35 ; Search time 17 Seconds
(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLVWGLMGLSCL.....DDLMEKSPRMESNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 6

Total number of hits satisfying chosen parameters: 905

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	1 PTHR_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTHR_RAT	P70555 rattus norv
3	25	4.6	585	1 PTHR_DIDMA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTHR_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTHR_MOUSE	P41593 mus musculu
8	18	3.3	591	1 PTHR_RAT	P25961 rattus norv
9	18	3.3	593	1 PTHR_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	O46502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 GIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	457	1 VIPR_MELGA	Q91085 meleagris g
15	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
16	13	2.4	459	1 VIPR_MOUSE	P97751 mus musculu
17	13	2.4	459	1 VIPR_RAT	P30083 rattus norv
18	13	2.4	462	1 GIPR_MESAU	P43218 mesocricetu
19	12	2.2	466	1 GIPR_HUMAN	P48546 homo sapien
20	10	1.8	477	1 GLR_HUMAN	P47871 homo sapien
21	10	1.8	550	1 GLP2_RAT	Q920w0 rattus norv
22	10	1.8	553	1 GLP2_HUMAN	Q95838 homo sapien
23	9	1.7	437	1 VIPR_MOUSE	P41588 mus musculu
24	9	1.7	437	1 VIPR_RAT	P35000 rattus norv
25	9	1.7	438	1 VIPR_HUMAN	P41587 homo sapien
26	9	1.7	463	1 GLPI_HUMAN	P43220 homo sapien
27	9	1.7	463	1 GLPI_RAT	P32301 rattus norv
28	9	1.7	468	1 PACR_HUMAN	P41586 homo sapien
29	9	1.7	485	1 GLR_MOUSE	Q61606 mus musculu
30	9	1.7	485	1 GLR_RAT	P30082 rattus norv
31	9	1.7	489	1 GLPI_MOUSE	O35659 mus musculu
32	9	1.7	496	1 PACR_MOUSE	P70205 mus musculu
33	9	1.7	513	1 PACR_BOVIN	Q29627 bos taurus

RESULT 1

PTHR2_HUMAN STANDARD; PRT; 550 AA.

AC P49190;

DT 01-FEB-1996 (Rel. 33, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Parathyroid hormone receptor precursor (PTH2 receptor).

GN PTHR2.

OS Homo sapiens (Human).

OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=95318121; PubMed=7797535;

RA Usdin T.B., Gruber C., Bonner T.I.;

RT "Identification and functional expression of a receptor selectively

RT recognizing parathyroid hormone, the PTH2 receptor.";

RL J. Biol. Chem. 270:15455-15458(1995).

RN [2]

RP SEQUENCE OF 26-40 AND 306-550 FROM N.A.

RX MEDLINE=97079671; PubMed=8921382;

RA Usdin T.B., Modi W., Bonner T.I.;

RT "Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33

RT by fluorescence in situ hybridization.";

RL Genomics 37:140-141(1996).

CC -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE

CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE

CC ADENYLATE CYCLASE.

CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.

CC ALSO EXPRESSED IN THE TESTIS.

CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; U25128; AAC50157.1; -

CC EMBL; U47124; AAC50157.1; -

CC EMBL; U47129; AAC50767.1; -

CC EMBL; U47125; AAC50767.1; JOINED.

CC EMBL; U47126; AAC50767.1; JOINED.

CC EMBL; U47127; AAC50767.1; JOINED.

CC EMBL; U47128; AAC50767.1; JOINED.

CC PIR; A57519; A57519.

CC Genew; HGNC:9609; PTHR2.

CC MIW; 601469; -

CC GO; GO:0005887; C:integral to plasma membrane; TAS.

CC GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.

CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

P32215 rattus norv
P28217 styela pilic
Q13324 homo sapien
P47866 rattus norv
P42784 synchococc
O46603 xenopus lae
P35347 mus musculu
P35353 rattus norv
O62772 ovis aries
O42602 xenopus lae
Q90812 gallus gall
Q60748 mus musculu

ALIGNMENTS

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

 EMBL; U20178; AAC50106.1; --
 EMBL; U28281; AAA87556.1; --
 EMBL; U13989; AAA64949.1; --
 EMBL; AB065660; BAC05886.1; --
 PIR; JC2532; JC2532.
 Genew; HGNC:10608; SCTR.
 MIM; 182098; --
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0015055; F:secretin receptor activity; TAS.
 GO; GO:0007586; P:digestion; TAS.
 GO; GO:0007588; P:excretion; TAS.
 GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
 InterPro; IPR000832; GPCR secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm_2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 440 SECRETIN RECEPTOR.
 FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 240 3 (POTENTIAL).
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 276 4 (POTENTIAL).
 FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 317 5 (POTENTIAL).
 FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 362 6 (POTENTIAL).
 FT DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 370 392 7 (POTENTIAL).
 FT DOMAIN 393 440 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 124 124 G -> A (IN REF. 1).
 FT CONFLICT 210 210 A -> P (IN REF. 2).
 FT CONFLICT 308 308 I -> F (IN REF. 3).
 FT CONFLICT 333 333 E -> Q (IN REF. 3).
 FT CONFLICT 377 377 G -> A (IN REF. 1).
 SQ SEQUENCE 440 AA; 50206 MW; E22CDD0BE7C0AC1 CRC64;
 Query Match 3.5%; Score 19; DB 1; Length 440;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 FRELHCTRYIHMHFLVSP 187
 |||||
 DB 167 FRELHCTRYIHMHFLVSP 185

RESULT 5

SCRC_RAT

ID_SCRC_RAT

STANDARD; PRT; 449 AA.

P23811;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Secretin receptor precursor (SCT-R).
 GN SCTR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=91266890; PubMed=1646711;
 RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
 RA Nagata S.;
 RT "Molecular cloning and expression of a cDNA encoding the secretin
 receptor.";
 RL EMBO J. 10:1635-1641(1991).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X59132; CAA41849.1; --
 PIR; S16319; S16319. GPCR secretin.
 InterPro; IPR000832; GPCR secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm_2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 449 SECRETIN RECEPTOR.
 FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 167 1 (POTENTIAL).
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 194 2 (POTENTIAL).
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 217 240 3 (POTENTIAL).
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 276 4 (POTENTIAL).
 FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 317 5 (POTENTIAL).
 FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 344 362 6 (POTENTIAL).
 FT DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 370 392 7 (POTENTIAL).
 FT DOMAIN 393 449 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;

Query Match

3.5%; Score 19; DB 1; Length 449;

Best Local Similarity 100.0%; Pred. No. 3.1e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLFVSP 187
 DB 167 FRLHCTRNVIHMLFVSP 185

RESULT 6

PTRR_PIG STANDARD; PRT; 585 AA.
 AC P50133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHr receptor).
 GN PTHR1 OR PTHR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]_SEQUENCE FROM N.A.

RP MEDLINE=96305358; PubMed=8688470;
 RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
 RA Chandrasekhar S., Hsiung H.M.;
 RT "Structure and functional expression of a complementary DNA for
 RT porcine parathyroid hormone/parathyroid hormone-related peptide
 RT receptor.";
 RL Biochim. Biophys. Acta 1307:339-347(1996).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; U18315; AAC48619.1; -.
 CC HSP; Q03431; 1BL1.
 CC InterPro; IPR000832; GPCR secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 CC PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 CC PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 26
 CC CHAIN 27 585
 CC PARATHYROID HORMONE/PARATHYROID HORMONE-
 CC RELATED PEPTIDE RECEPTOR.
 CC EXTRACELLULAR (POTENTIAL).
 CC 1 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 2 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 3 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 4 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 5 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 6 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 424 435

FT TRANSMEM 436 458 7 (POTENTIAL).
 FT DOMAIN 459 585 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 48 113 BY SIMILARITY.
 FT DISULFID 104 144 BY SIMILARITY.
 FT DISULFID 127 166 BY SIMILARITY.
 FT CARBOHYD 147 172 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 157 172 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 162 172 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 585;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
 DB 285 YFLATNYWILVEGLYLH 302

RESULT 7

PTRR_MOUSE STANDARD; PRT; 591 AA.
 AC P41593; Q62119;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHr receptor).
 GN PTHR1 OR PTHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN=C3H/HEHA;
 RC MEDLINE=95034305; PubMed=7524627;
 RA Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,
 RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
 RT "Expression pattern of parathyroid hormone/parathyroid hormone
 RT related peptide receptor mRNA in mouse postimplantation embryos
 RT indicates involvement in multiple developmental processes.";
 RL Mech. Dev. 47:29-42(1994).
 RN [2]_SEQUENCE FROM N.A.

RP STRAIN=BALB/c;
 RC MEDLINE=942553468; PubMed=8197183;
 RA McCuaig K.A., Clarke J.C., White J.H.;
 RT "Molecular cloning of the gene encoding the mouse parathyroid
 RT hormone/parathyroid hormone-related peptide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; X78936; CAA55536.1; -.
 CC EMBL; L34611; AAA40011.1; -.
 CC EMBL; L34608; AAA40011.1; JOINED.
 CC EMBL; L34607; AAA40011.1; JOINED.
 CC EMBL; L34609; AAA40011.1; JOINED.

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;
 Query Match 3.3%; Score 18; DB 1; Length 591;
 Best Local Similarity 100.0%; Pred. No. 4.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 YFLATNYWYILVEGLYLH 262
 DB 290 YFLATNYWYILVEGLYLH 307

RESULT 9
 PTHR HUMAN STANDARD; PRT; 593 AA.
 AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHrP receptor).
 GN PTHrP OR PTHR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93238641; PubMed=8386612;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RL Endocrinology 132:2157-2165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93387403; PubMed=8397094;
 RA Schneider H., Feyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263723; PubMed=7745008;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.P.,
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Juppner H.;
 RT "Pseudohypoparathyroidism type Ib is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=20374568; PubMed=10913300;
 RA Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schafer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 168-198.

RA MEDLINE=98409426; PubMed=9737850;
 RX Pellegrini M., Biello A., Rosenblatt M., Chorev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT MURK-JANSEN ARG-223.
 RX MEDLINE=95215874; PubMed=7701349;
 RA Schipani E., Kruse K., Juppner H.;
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=8703170;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Juppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL New Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP MUTAGENESIS OF ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745;
 RA Schipani E., Jensen G.S., Pincus J., Nissen R.A., Gardella T.J.,
 RA Juppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
 CC SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
 CC KIDNEY, BONE AND LIVER.
 CC -!- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF BLOWSTRAND TYPE OF
 CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
 CC -!- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF MURK-JANSEN TYPE OF
 CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
 CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
 CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
 CC HORMONES.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L04308; AAA36525.1; -.
 CC EMBL; X68596; CAA48589.1; -.
 CC EMBL; U22409; AAB60657.1; -.
 CC EMBL; U22401; AAB60657.1; JOINED.
 CC EMBL; U22402; AAB60657.1; JOINED.
 CC EMBL; U22403; AAB60657.1; JOINED.
 CC EMBL; U22404; AAB60657.1; JOINED.
 CC EMBL; U22405; AAB60657.1; JOINED.
 CC EMBL; U22406; AAB60657.1; JOINED.
 CC EMBL; U22407; AAB60657.1; JOINED.
 CC EMBL; U22408; AAB60657.1; JOINED.
 CC EMBL; U17418; AAA56774.1; -.
 CC PIR; I38139; A49191.
 CC PDB; 1BL1; 30-MAR-99.
 CC PDB; 1ET2; 06-SEP-00.
 CC PDB; 1ET3; 06-SEP-00.
 CC Genew; HGNC:9608; PTHrP.

15-JUL-1999 (Rel. 38, last sequence update)
16-OCT-2001 (Rel. 40, last annotation update)
Secretin receptor precursor (SCT-R).
SCTR.
Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98366112; PubMed=9700755;
RA Svoboda M., Tastenoy M., de Neef P., Delporte C., Waelbroeck M.,
RA Robberecht P.;
RT "Molecular cloning and in vitro properties of the recombinant rabbit
secretin receptor.";
RL Peptides 19:1055-1062(1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF025411; AAC32767.1; -
DR InterPro: IPR000832; GPCR secretin.
DR InterPro: IPR001879; hormn_receptor.
DR Pfam: PF00002; 7tm_2; 1.
DR Pfam: PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1
DR PROSITE; PS00649; G-PROTEIN RECP F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN RECP F2_2; 1.
DR PROSITE; PS00227; G-PROTEIN RECP F2_3; 1.
DR PROSITE; PS00261; G-PROTEIN RECP F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 445 SECRETIN RECEPTOR.
FT DOMAIN 22 139 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 140 163 1 (POTENTIAL).
FT DOMAIN 164 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 190 2 (POTENTIAL).
FT DOMAIN 191 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 236 3 (POTENTIAL).
FT DOMAIN 237 250 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 251 272 4 (POTENTIAL).
FT DOMAIN 273 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 313 5 (POTENTIAL).
FT DOMAIN 314 339 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 358 6 (POTENTIAL).
FT DOMAIN 359 365 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 366 388 7 (POTENTIAL).
FT DOMAIN 389 445 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;

Query Match 3.0%; Score 16; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHMLF 184
|||
Db 163 FRLHCTRNVIHMLF 178
|||

RESULT 11

ID	VIPR_CARAU	STANDARD;	PRT;	447 AA.
AC	Q90308;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Vasodilative intestinal polypeptide receptor (VIP-R) (VIP receptor).			
OS	Carassius auratus (Goldfish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Carassius.			
OX	NCBI_TaxID=7957;			
RI	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97190233; PubMed=9038250;			
RA	Chow B.K.C., Yuen T.T.H., Chan K.W.;			
RT	"Molecular evolution of vertebrate VIP receptors and functional			
RT	characterization of a VIP receptor from goldfish Carassius auratus."			
RL	Gen. Comp. Endocrinol. 105:1176-185(1997).			
CC	-I- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS			
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL			
CC	CYCLASE.			
CC	CELLULAR LOCATION: Integral membrane protein.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL	U56391; AAB05459.1; -			
DR	InterPro: IPR000832; GPCR secretin.			
DR	InterPro: IPR001879; hormm_receptor.			
DR	Pfam: PF00002; 7tm_2; 1.			
DR	Pfam: PF02793; HRM; 1			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	SMART; SM00008; Hormr; 1.			
DR	PROSITE; PS00649; G_PROTEIN_REC_P2_1; 1.			
DR	PROSITE; PS00650; G_PROTEIN_REC_P2_2; 1.			
DR	PROSITE; PS0227; G_PROTEIN_REC_P2_3; 1.			
DR	PROSITE; PS0241; G_PROTEIN_REC_P2_4; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 103			
FT	TRANSMEM 104 128			
FT	DOMAIN 129 135			
FT	TRANSMEM 136 155			
FT	DOMAIN 156 178			
FT	TRANSMEM 179 202			
FT	DOMAIN 203 216			
FT	TRANSMEM 217 238			
FT	DOMAIN 239 256			
FT	TRANSMEM 257 280			
FT	DOMAIN 281 305			
FT	TRANSMEM 306 325			
FT	DOMAIN 326 337			
FT	TRANSMEM 338 357			
FT	DOMAIN 358 447			
FT	DISULFID 177 247			
FT	CARBOHYD 17 17			
FT	CARBOHYD 22 22			
FT	CARBOHYD 64 64			
FT	CARBOHYD 91 91			
FT	CARBOHYD 169 169			
SEQ	SEQUENCE 447 AA; 50959 MW; 66839E243702554C SRC64;			

Query Match 3.0%; Score 16; DB 1; Length 447;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT DOMAIN 317 338 CYTOPLASMIC (POTENTIAL) .
 FT TRANSMEM 339 359 6 (POTENTIAL) .
 FT DOMAIN 360 374 EXTRACELLULAR (POTENTIAL) .
 FT TRANSMEM 375 395 7 (POTENTIAL) .
 FT DOMAIN 396 455 CYTOPLASMIC (POTENTIAL) .
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL) .
 SQ SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNTHM 181
 |||||
 DB 159 FRLHCTRNTHM 171
 |||||

RESULT 13
 VIPR HUMAN STANDARD; PRT; 457 AA.
 AC P22241; Q15871; 27, Created
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Homo sapiens (Human) .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=9320641; PubMed=8390245;
 RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;
 RT "Cloning and functional expression of a human neuroendocrine
 RT vasoactive intestinal peptide receptor.";
 RL Biochem. Biophys. Res. Commun. 193:546-553 (1993) .
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Intestine;
 RX MEDLINE=94235025; PubMed=8179610;
 RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,
 RA Ogier-Denis E., Laburthe M.;
 RT "Human intestinal VIP receptor: cloning and functional expression of
 RT two cDNA encoding proteins with different N-terminal domains.";
 RL Biochem. Biophys. Res. Commun. 200:769-776 (1994) .
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tsuta M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsubumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 RT receptor genes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 33-457 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=95001220; PubMed=7917790;
 RA Gagnon A.W., Aivar N., Elshourbagy N.A.;
 RT "Molecular cloning and functional characterization of a human liver
 RT vasoactive intestinal peptide receptor.";
 RL Cell. Signal. 6:321-333 (1994) .
 RN [5]
 RP DISULFIDE BOND.
 RX MEDLINE=99126981; PubMed=9928020;
 RA Knudsen S.M., Tams J.W., Wulff B.S., Fahrenkrug J.;
 RT "Importance of conserved cysteines in the extracellular loops of
 RT human PACAP/VIP1 receptor for ligand binding and stimulation of cAMP
 RT production.";

RL Ann. N.Y. Acad. Sci. 865:259-265 (1998).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Bvnt=Alternative splicing; Named isoforms=2;
 CC Name=Short; Synonyms=hivR8;
 CC IsoId=P32241-1; Sequence=Displayed;
 CC Name=Long; Synonyms=hivR5;
 CC IsoId=P32241-2; Sequence=VSP_002010;
 CC -1- TISSUE SPECIFICITY: IN LUNG, HF29 COLONIC EPITHELIAL CELLS, RAJI
 CC B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY, LIVER AND
 CC PLACENTA.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U11087; AAB60362.1; -
 CC EMBL; U11079; AAB60362.1; JOINED.
 CC EMBL; U11080; AAB60362.1; JOINED.
 CC EMBL; U11081; AAB60362.1; JOINED.
 CC EMBL; U11083; AAB60362.1; JOINED.
 CC EMBL; U11084; AAB60362.1; JOINED.
 CC EMBL; U11085; AAB60362.1; JOINED.
 CC EMBL; U11086; AAB60362.1; JOINED.
 CC EMBL; L13288; AAA36805.1; -
 CC EMBL; X77777; CAA54814.1; -
 CC EMBL; X75299; CAA53046.1; -
 CC EMBL; AB065669; BAC05895.1; -
 CC EMBL; L20295; AAA36802.1; -
 CC PIR; JC2194; JC2194.
 CC Genew; HGNC:12694; VIPR1.
 CC MIM; 192321; -
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004999; F:vasoactive intestinal polypeptide receptor . . ; TAS.
 CC GO; GO:0007586; P:digestion; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . . ; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC GO; GO:0006936; P:muscle contraction; TAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC GO; GO:0007268; P:synaptic transmission; TAS.
 CC InterPro; IPR000832; GPCR_secretin.
 CC InterPro; IPR001879; hormn_receptor.
 CC Pfam; PF00002; 7tm_2; 1.
 CC Pfam; PF02793; HRM; 1.
 CC PRINTS; PR00249; GPCRSECRETIN.
 CC SMART; SM00008; Hormr; 1.
 CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 CC PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 CC PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Alternative splicing
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 457 VASOACTIVE INTESTINAL POLYPEPTIDE
 FT RECEPTOR 1.
 FT DOMAIN 31 142 EXTRACELLULAR (POTENTIAL) .
 FT TRANSMEM 143 167 1 (POTENTIAL) .
 FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL) .
 FT TRANSMEM 175 194 2 (POTENTIAL) .
 FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL) .
 FT TRANSMEM 217 240 3 (POTENTIAL) .
 FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL) .
 FT TRANSMEM 255 276 4 (POTENTIAL) .
 FT DOMAIN 277 292 EXTRACELLULAR (POTENTIAL) .
 FT TRANSMEM 293 316 5 (POTENTIAL) .


```
CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U49434; AAA93390.1; -.
CC InterPro; IPR000832; GPCR_secretin.
CC InterPro; IPR001879; hormn_receptor.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; Hormr; 1.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
CC PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 31
CC CHAIN 32 458
CC VASOACTIVE INTESTINAL POLYPEPTIDE
CC RECEPTOR 1.
CC DOMAIN 32 143
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 144 168
CC 1 (POTENTIAL).
CC DOMAIN 169 175
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 176 195
CC 2 (POTENTIAL).
CC DOMAIN 196 217
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 218 241
CC 3 (POTENTIAL).
CC DOMAIN 242 255
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 256 277
CC 4 (POTENTIAL).
CC DOMAIN 278 293
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 294 317
CC 5 (POTENTIAL).
CC DOMAIN 318 342
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 343 362
CC 6 (POTENTIAL).
CC DOMAIN 363 374
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 375 394
CC 7 (POTENTIAL).
CC DOMAIN 395 458
CC CYTOPLASMIC (POTENTIAL).
CC DISULFID 216 286
CC BY SIMILARITY.
CC CARBOHYD 59 59
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 70 70
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 101 101
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 105 105
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 458 AA; 51479 MW; E166E4D6B3BE1189 CRC64;
```

Query Match 2.4%; Score 13; DB 1; Length 458;

Best Local Similarity 100.0%; Pred. No. 4.6e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHMLF 184

|||||

Db 171 LHCTRYIHMLF 183

Search completed: November 21, 2003, 22:34:29

Job time : 17 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:28:00 ; Search time 47 seconds

(without alignments)
1827.044 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLWGMLGSL.....DDLMEKFSRPMESNPDTEG 541

Scoring table: OLIGO

Gap 60.0 , Gapext 50.0

Searched: 1107863 seqs, 158726573 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	AA112695	G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hypophosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolisis; therapy; diagnosis.
2	363	67.1	550	AA112695	Human PTR2 seven t
3	363	67.1	550	AA112695	Lung cancer-associ
4	363	67.1	550	AA112695	Human parathyroid
5	342	63.2	561	AA112695	Lung cancer-associ
6	262	48.4	550	AA112695	Non-endogenous hum
7	262	48.4	550	AA112695	Human PTH2 receptor
8	38	7.0	546	AA112695	Rat PTH2 receptor
9	25	4.6	515	AA112695	Opessum kidney PTH

10	25	4.6	515	17	AA112695	Opessum kidney PTH
11	25	4.6	515	13	AA112695	Parathyroid hormone
12	25	4.6	585	13	AA112695	Opessum kidney PTH
13	25	4.6	585	17	AA112695	Opessum kidney PTH
14	25	4.6	585	20	AA112695	Parathyroid hormone
15	22	4.1	864	22	AA112695	Novel human diagno
16	20	3.7	20	24	AA112695	G protein-coupled
17	19	3.5	440	21	AA112695	Amino acid sequenc
18	19	3.5	440	22	AA112695	Non-endogenous hum
19	19	3.5	440	22	AA112695	Human SCRC seven t
20	19	3.5	440	23	AA112695	Protein identified
21	19	3.5	440	23	AA112695	Human secretin rec
22	19	3.5	440	24	AA112695	Human secretin rec
23	19	3.5	449	13	AA112695	Secretin receptor
24	18	3.3	18	24	AA112695	G protein-coupled
25	18	3.3	324	21	AA112695	Tethered PTH-1 rec
26	18	3.3	335	21	AA112695	Tethered PTH-1 rec
27	18	3.3	435	21	AA112695	Human tethered PTH
28	18	3.3	435	21	AA112695	A mutant parathyro
29	18	3.3	446	21	AA112695	Tethered PTH-1 rec
30	18	3.3	448	21	AA112695	Human tethered PTH
31	18	3.3	450	21	AA112695	Human tethered PTH
32	18	3.3	536	21	AA112695	Zebrafish parathyr
33	18	3.3	536	21	AA112695	Rat bone PTH/PTHrP
34	18	3.3	591	13	AA112695	Rat bone PTH/PTHrP
35	18	3.3	591	17	AA112695	Parathyroid hormone
36	18	3.3	591	20	AA112695	Human kidney PTH/P
37	18	3.3	593	17	AA112695	Human Parathyroid
38	18	3.3	593	20	AA112695	Non-endogenous hum
39	18	3.3	593	22	AA112695	Human PTR2 seven t
40	18	3.3	593	22	AA112695	Human parathyroid
41	18	3.3	593	24	AA112695	Canine parathyroid
42	18	3.3	595	24	AA112695	Human kidney PTH/P
43	18	3.3	614	13	AA112695	Carassius auratus
44	16	3.0	447	23	AA112695	PTH/PTHrP receptor
45	14	2.6	19	13	AA112695	

ALIGNMENTS

RESULT 1

AA112695
ID AA112695 standard; Protein; 541 AA.

XX AC AA112695;

XX AC AA112695;

XX DT 31-MAY-1997 (first entry)

XX DE G-protein parathyroid hormone receptor HLTG74.

XX DE G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH; calcium; signal transduction; agonist; antagonist; hypocalcaemia; hypophosphataemia; hypoparathyroidism; chronic tetany; osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia; kidney stone; nephrolisis; therapy; diagnosis.

XX OS Homo sapiens.

XX PN WO639433-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1995; 95WO-US07085.

XX PR 05-JUN-1995; 95WO-US07085.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX DR WPI; 1997-043068/04.

XX DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
XX Claim 9; Fig 1A-E; 62pp; English.
XX
CC A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AAT59619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphatemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphatemia, kidney stone, nephrolithiasis.
XX
XX SQ Sequence 541 AA;

Query Match 100.0%; Score 541; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSHVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQGE 60
DB 1 MAWLGLSHVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQGE 60
QY 61 GNCFFPDGLI CWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
DB 61 GNCFFPDGLI CWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
QY 121 NYSDDLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYH 180
DB 121 NYSDDLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYH 180
QY 181 MHLFVSFMLRATSI FVKDRVVAHI GVKELESIMQDDPQNSIEATSVKSYIGCKIAV 240
DB 181 MHLFVSFMLRATSI FVKDRVVAHI GVKELESIMQDDPQNSIEATSVKSYIGCKIAV 240
QY 241 VMFIYELATNYWILVEGLYLNLI FVAFSDTKYLWGFIILGWGPPAA FVAWAVARAT 300
DB 241 VMFIYELATNYWILVEGLYLNLI FVAFSDTKYLWGFIILGWGPPAA FVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
DB 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVFVGVHIVFVCLPHSFTGLGWEIRHCELFNSFQGFVSIICYCNGEV 420
DB 361 LAKSTLVLVFVGVHIVFVCLPHSFTGLGWEIRHCELFNSFQGFVSIICYCNGEV 420
QY 421 QAEVKKMSRWNLSDVWKETPPCGSRCCSVLTTHSTSSQSVAAAHAWCLSLAKLPR 480
DB 421 QAEVKKMSRWNLSDVWKETPPCGSRCCSVLTTHSTSSQSVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYAMSGVVTQSRATSLSTRNKEDSGRQDDILMEKPSRPWESNPDE 540
DB 481 SPADSLTATSLYAMSGVVTQSRATSLSTRNKEDSGRQDDILMEKPSRPWESNPDE 540
QY 541 G 541
DB 541 G 541

RESULT 2
AAB71875
ID AAB71875 standard; Protein; 550 AA.
XX
AC AAB71875;
XX

DT 03-MAY-2001 (first entry)
XX
DE Human PTH2 seven transmembrane domain.
XX
KW Human: PTH2; parathyroid hormone receptor; h15571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
KW graft rejection; cystic fibrosis.
XX
XX Homo sapiens.
OS
XX WO200109328-A1.
PN
XX 08-FEB-2001.
PD
XX 03-AUG-2000; 2000WO-US21278.
PF
XX 03-AUG-1999; 99US-0146916.
PR 29-FEB-2000; 2000US-0515781.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Hodge MR, Lloyd C, Weich NS;
PI
XX WPI; 2001-138653/14.
DR
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
PT
XX Disclosure; Fig 2; 145pp; English.
PS
XX The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.
XX
XX SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 22; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASHVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQGE 63
DB 4 LGASHVWGLMGLSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITAIQGE 63
QY 64 FPEWDGLICWRPGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANS 123
DB 64 FPEWDGLICWRPGTVGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWANS 123
QY 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183
DB 124 DCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183
QY 184 FVSFMLRATSI FVKDRVVAHI GVKELESIMQDDPQNSIEATSVKSYIGCKIAV 243
DB 184 FVSFMLRATSI FVKDRVVAHI GVKELESIMQDDPQNSIEATSVKSYIGCKIAV 243

QY 244 IYFLATNYIWLVEGLYLHNLIFVAFSDTKYLMGFILGWGPPAFVAAVARATLAD 303
Db 244 IYFLATNYIWLVEGLYLHNLIFVAFSDTKYLMGFILGWGPPAFVAAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWNATVAGHDTKQYKRLAK 363
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWNATVAGHDTKQYKRLAK 363
QY 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCHELFNSFGQFFVSIYCYCNGEVOAE 423
Db 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCHELFNSFGQFFVSIYCYCNGEVOAE 423
QY 424 VKKWSRWNLSDWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467
Db 424 VKKWSRWNLSDWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467

RESULT 3
ABU56732

ID ABU56732 standard; Protein; 550 AA.
XX AC ABU56732;
XX DT 02-APR-2003 (first entry)
XX DE Lung cancer-associated polypeptide #325.
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

OS WO200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

XX 10-MAY-2001; 2001US-290492P.

XX 09-NOV-2001; 2001US-339245P.

XX 13-NOV-2001; 2001US-350666P.

XX 29-NOV-2001; 2001US-334370P.

XX 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

XX N-PSDB; ABX76461.

PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -

XX Claim 27; Page 439-440; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung
XX cancer-associated polynucleotides and polypeptides are used for
XX identifying a compound that modulates a lung cancer-associated
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX cell to treat lung cancer in a patient and for treating a mammal having
XX lung cancer by administering a modulatory compound identified. The
XX methods are useful for treating lung cancer, such as small cell lung

CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
CC polypeptides of the invention.

XX Sequence 550 AA;

Query Match

Best Local Similarity 67.1%; Score 363; DB 24; Length 550;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHVWGWLMLGSLARALQDSDGTTTTEEQIVLVLKAKVOCELNITAIQOEGNC 63
Db 4 LGASLHVWGWLMLGSLARALQDSDGTTTTEEQIVLVLKAKVOCELNITAIQOEGNC 63
QY 64 PPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWANYS 123
Db 64 PPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSINKTWANYS 123
QY 124 DCLRFLOPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRHLCTRNYIHML 183
Db 124 DCLRFLOPDISIGKOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRHLCTRNYIHML 183
QY 184 FVSPMLRATSIYFVKDVRVVAHIGVKELESIMODDPQNSIATSVKSYIGCKIAVWVF 243
Db 184 FVSPMLRATSIYFVKDVRVVAHIGVKELESIMODDPQNSIATSVKSYIGCKIAVWVF 243
QY 244 IYFLATNYIWLVEGLYLHNLIFVAFSDTKYLMGFILGWGPPAFVAAVARATLAD 303
Db 244 IYFLATNYIWLVEGLYLHNLIFVAFSDTKYLMGFILGWGPPAFVAAVARATLAD 303
QY 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWNATVAGHDTKQYKRLAK 363
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWNATVAGHDTKQYKRLAK 363
QY 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCHELFNSFGQFFVSIYCYCNGEVOAE 423
Db 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCHELFNSFGQFFVSIYCYCNGEVOAE 423
QY 424 VKKWSRWNLSDWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467
Db 424 VKKWSRWNLSDWKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467

RESULT 4

ABP81871

ID ABP81871 standard; Protein; 550 AA.

XX AC ABP81871;

XX DT 04-MAR-2003 (first entry)

XX Human parathyroid hormone receptor 2 protein SEQ ID NO:227.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

XX Homo sapiens.

XX WO200261087-A2.

XX PN

XX 08-AUG-2002.
 XX 19-DEC-2001; 2001WO-US50107.
 XX 19-DEC-2000; 2000US-257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX N-PSDB; ABZ42718.
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 XX (GPCR), useful for diagnosing and designing drugs for treating
 XX conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 XX cancer or autoimmune diseases -
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising:
 XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular
 XX G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity
 XX or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 XX in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 XX an antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting the
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCRs and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related diseases, immunological-related cell proliferative
 XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
 XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
 XX disease, Parkinson's disease, multiple sclerosis, psoriasis,
 XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
 XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 XX any other disorder in which GPCRs are involved. The antibodies may be
 XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 XX GPCR proteins given in ABP81675 to ABP82019, which are used in the
 XX exemplification of the present invention.
 XX Sequence 550 AA;
 Query Match 67.1%; Score 363; DB 24; Length 550;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 LGASHVWGMLMGSLARALQSDGTITTEEQIVLVKAKVQCELNITAQLEGSGNC 63
 DB 4 LGASHVWGMLMGSLARALQSDGTITTEEQIVLVKAKVQCELNITAQLEGSGNC 63
 QY 64 PFEWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFFHCNPNGTWDFMGLNKTWANY 123
 DB 64 PFEWGLICWPRGTGKISAVPCPPYIYDFNHKGVAFFHCNPNGTWDFMGLNKTWANY 123
 QY 124 DCLRFLOPDISIGKQEFERLYVMYTVGYSISFGSLAVAILIIGVFRHLHCTRYIHMHL 183
 DB 124 DCLRFLOPDISIGKQEFERLYVMYTVGYSISFGSLAVAILIIGVFRHLHCTRYIHMHL 183
 QY 184 FVSFMLRATSPVKDRVVHAHGVKLESLIMQDDPQNSIEATSVDSQVIGCKIAYVMF 243
 DB 184 FVSFMLRATSPVKDRVVHAHGVKLESLIMQDDPQNSIEATSVDSQVIGCKIAYVMF 243
 QY 244 IYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLIFILGFGFPAAFVAAVARATLAD 303
 DB 244 IYFLATNYWILVEGLYHLNLIIFVAFPSDTKYLWGLIFILGFGFPAAFVAAVARATLAD 303

QY 304 ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVVRVLAATKIWNENAVGHDTKQYRKLAK 363
 DB 304 ARCWELSAGDIKWIYQAPILAAIGLNFILFLNTVVRVLAATKIWNENAVGHDTKQYRKLAK 363
 QY 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWETRMHCHLFPNSFQGFVSIYCYNGEVOAE 423
 DB 364 STLVLVLVFGVHYIYFVCLPHSFTGLGWETRMHCHLFPNSFQGFVSIYCYNGEVOAE 423
 QY 424 VKKWSRNWLSVDWKRTPPCGSRRCGSLVLTITVTHSTSSQSQVAA 467
 DB 424 VKKWSRNWLSVDWKRTPPCGSRRCGSLVLTITVTHSTSSQSQVAA 467

RESULT 5
 ABUS6731
 ID ABUS6731 standard; Protein; 561 AA.
 XX AC ABUS6731;
 XX 02-APR-2003 (first entry)
 XX Lung cancer-associated polypeptide #324.
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 XX WO200286443-A2.
 XX 31-OCT-2002.
 XX 18-APR-2002; 2002WO-US12476.
 XX 18-APR-2001; 2001US-284770P.
 XX 10-MAY-2001; 2001US-290492P.
 XX 09-NOV-2001; 2001US-339245P.
 XX 13-NOV-2001; 2001US-350666P.
 XX 29-NOV-2001; 2001US-334370P.
 XX 12-APR-2002; 2002US-372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Aziz N, Murray R;
 XX WPI; 2003-093161/08.
 XX N-PSDB; ABX76460.
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 XX for treating lung cancer, by contacting a biological sample from the
 XX patient with a polynucleotide that exhibits increased or decreased
 XX expression in lung cancer -
 XX Claim 27; Page 439; 453pp; English.
 XX The invention relates to a method for detecting a lung cancer-associated
 XX transcript in a cell from a patient, comprising contacting a biological
 XX sample from the patient with a polynucleotide that selectively hybridises
 XX to a sequence that is at least 80 % identical to a gene that exhibits
 XX increased or decreased expression in lung cancer samples. Lung
 XX cancer-associated polynucleotides and polypeptides are used for
 XX identifying a compound that modulates a lung cancer-associated
 XX polypeptide, for inhibiting proliferation of a lung cancer-associated
 XX cell to treat lung cancer in a patient and for treating a mammal having
 XX lung cancer by administering a modulatory compound identified. The
 XX methods are useful for treating lung cancer, such as small cell lung
 XX cancer, non-small cell lung cancer or other benign or precancerous
 XX lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 XX pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 XX pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides

KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Homo sapiens.
 XX WO2000077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig 1; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cyostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX Sequence 550 AA;
 SQ Query Match 48.4%; Score 262; DB 22; Length 550;
 Best Local Similarity 99.6%; Pred. No. 2.1e-259;
 Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LGASHVWGMVLMGSCLLARQLQSDGTITIEEIVLVKAKVOCELNITAOIQEGEGNC 63
 DB 4 LGASHVWGMVLMGSCLLARQLQSDGTITIEEIVLVKAKVOCELNITAOIQEGEGNC 63
 QY 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRCHNPNGTWDFMELNKTWANY 123
 DB 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRCHNPNGTWDFMELNKTWANY 123
 QY 124 DCLRLQPDISIGQKQFCEFLYVMYTVGYSISFSGSLAVAILIGYFRLHCTRYIHML 183
 DB 124 DCLRLQPDISIGQKQFCEFLYVMYTVGYSISFSGSLAVAILIGYFRLHCTRYIHML 183
 QY 184 FVSEMLRATSFVKDRVVAHIGVKELESIMQDDPQNSTEATSVDSKQVIGCKIAVWF 243
 DB 184 FVSEMLRATSFVKDRVVAHIGVKELESIMQDDPQNSTEATSVDSKQVIGCKIAVWF 243
 QY 244 IYFLATNYIWLVEGLYLNHIFVAFFSDTKYLMGFIILGFGFPAAPFAVAWAVARATLAD 303
 DB 244 IYFLATNYIWLVEGLYLNHIFVAFFSDTKYLMGFIILGFGFPAAPFAVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWYIQAPILAAIGLNFILFVLTNVRVLAATKIWETNAVGHTRKQYKLA 363

DB 304 ARCWELSGADIKWYIQAPILAAIGLNFILFVLTNVRVLAATKIWETNAVGHTRKQYKLA 363
 QY 364 STLVLVLVFGVHYIVFVCLPHSFITGLQWEIRMHCELFNSFQGFVSIICYCNGEQAE 423
 DB 364 STLVLVLVFGVHYIVFVCLPHSFITGLQWEIRMHCELFNSFQGFVSIICYCNGEQAE 423
 QY 424 VKQWMSRWNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQSVAA 467
 DB 424 VKQWMSRWNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQSVAA 467
 XX RESULT 8
 XX AAB80559
 XX ID AAB80559 standard; Protein; 546 AA.
 XX AC AAB80559;
 XX 26-APR-2001 (first entry)
 XX Rat PTH2 receptor amino acid sequence.
 XX Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
 KW cyostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 XX Rattus sp.
 XX WO2000077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig 1; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiant, cyostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.

SQ Sequence 546 AA;

Query Match 7.0%; Score 38; DB 22; Length 546;
 Best Local Similarity 100.0%; Pred. No. 8.5e-30;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILNTVRVLATKIWETNAVCHD 353
 |||||
 Db 313 WIYQAPILAAIGLNFILNTVRVLATKIWETNAVCHD 350

RESULT 9

AAR27704
 ID AAR27704 standard; Protein; 515 AA.

XX AAR27704;

XX 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)

XX Opossum kidney PTH/PTHrP receptor prep'd. from clone OK-H.

XX DE Parathyroid hormone; related protein; calcium; antagonist;
 XX KW antibodies; hypercalcaemia.

XX Didelphis virginiana.

XX WO9217602-A1.

XX 15-OCT-1992.

XX 06-APR-1992; 92WO-US02821.

XX 05-APR-1991; 91US-0681702.

XX 06-APR-1992; 92US-0864475.

XX (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani B;
 FI Segre GV;

XX N-PSDB; 1992-366271/44.
 DR N-PSDB; AAQ29604.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours

XX Disclosure; Fig 1; 91pp; English.

XX The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor protein sequence was deduced from the DNA sequence of the
 CC clone OK-H, isolated from opossum kidney (OK) cells. The protein
 CC may be used in a therapeutic compsn. to inhibit activation of PTH or
 CC PTHrP and thus reduce the level of calcium in the blood. Cpd.
 CC capable of competing with PTH or PTHrP for binding can be identified
 CC using the protein prod. and DNAs homologous to PTH DNA can be
 CC identified using fragments of the clone as probes. The protein
 CC may be used for the prodn. of antibodies useful for the treatment,
 CC classification, prognosis and/or treatment of disorders related to
 CC the interaction between a cell receptor and a ligand such as in
 CC hypercalcaemia. See also AAR27705-16.
 CC (Updated on 25-MAR-2003 to correct FN field.)

SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 13; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYNHMLFVSVFMLRA 191

|||||
 Db 207 GYFRRLHCTRYNHMLFVSVFMLRA 231

RESULT 10

AAR92275
 ID AAR92275 standard; Protein; 515 AA.

XX AAR92275;

XX 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)

XX Opossum kidney PTH/PTHrP receptor.

XX KW Parathyroid hormone; receptor; parathormone; PTH;
 XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 XX KW hypercalcaemia; hypocalcaemia; cancer; opossum.

XX Didelphis virginiana.

XX US5494806-A.

XX 27-FEB-1996.

XX 06-APR-1992; 92US-0864475.

XX 06-APR-1992; 92US-0864475.

XX 05-APR-1991; 91US-0681702.

XX (GEO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 FI Schipani B, Segre GV;

XX WPI; 1996-139028/14.

XX N-PSDB; AAT15945.

XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.

XX Claim 1; Fig 1A-1E; 64pp; English.

XX Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC kidney (OK) and OK-O (AAT15946), respectively, isolated from an opossum
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 17; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRYNHMLFVSVFMLRA 191

|||||
 Db 207 GYFRRLHCTRYNHMLFVSVFMLRA 231

RESULT 11

AAW73314
 ID AAW73314 standard; Protein; 515 AA.

XX AAW73314;

XX 08-FEB-1999 (first entry)

XX Parathyroid hormone receptor OK-H.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5840853-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 06-JUN-1995; 95US-0471494.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX
 DR WPI; 1999-034124/03.
 DR N-PSDB; AAV08388.
 XX
 PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX
 PS Claim 6; Fig 1; 63pp; English.
 XX
 CC This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-H, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 515 AA;
 Query Match 4.6%; Score 25; DB 20; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.7e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLHCTRNYYIHMHFLVFSFMLRA 191
 |||||
 DB 207 GYFRRLHCTRNYYIHMHFLVFSFMLRA 231
 |||||
 RESULT 12
 AAR27705
 ID AAR27705 standard; Protein; 585 AA.
 XX
 AC AAR27705;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-MAR-1993 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
 XX
 KW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia.
 XX
 OS Didelphis virginiana.
 XX
 PN WO9217602-A1.
 PN
 PD 15-OCT-1992.
 XX
 PF 06-APR-1992; 92WO-US02821.
 XX
 PR 05-APR-1991; 91US-0681702.
 PR 06-APR-1992; 92US-0864475.

XX
 PA (GEHO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX
 PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;
 XX
 DR WPI; 1992-366271/44.
 DR N-PSDB; AAQ29605.
 XX
 PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours
 XX
 PS Disclosure; Fig 2; 91pp; English.
 XX
 CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
 CC receptor protein sequence was deduced from the DNA sequence of the
 CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
 CC is identical to the OK-H clone except at the C-terminal tail as OK-O
 CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
 CC The difference is attributed to a single nucleotide deleted in the OK-H
 CC sequence causing a frame shift and an earlier stop codon. It is not
 CC known whether OK-O and OK-H represent prods. of two separate genes or
 CC are a laboratory artifact. The protein may be used in a therapeutic
 CC compsn. to inhibit activation of PTH or PTHrP and thus reduce the
 CC level of calcium in the blood. Cpd. capable of competing with PTH
 CC or PTHrP for binding can be identified using the protein prod. and
 CC DNAs homologous to PTH DNA can be identified using fragments of the
 CC clone as probes. The sequence may be used for the prodn. of antibodies
 CC useful for the treatment, classification, prognosis and/or treatment of
 CC disorders related to the interaction between a cell receptor and a
 CC ligand such as in hypercalcaemia. See also AAR27704-16.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 585 AA;
 Query Match 4.6%; Score 25; DB 13; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRRLHCTRNYYIHMHFLVFSFMLRA 191
 |||||
 DB 207 GYFRRLHCTRNYYIHMHFLVFSFMLRA 231
 |||||
 RESULT 13
 AAR92276
 ID AAR92276 standard; Protein; 585 AA.
 XX
 AC AAR92276;
 XX
 DT 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)
 XX
 DE Opossum kidney PTH/PTHrP receptor.
 XX
 KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer; opossum.
 XX
 OS Didelphis virginiana.
 XX
 PN US5494806-A.
 XX
 PD 27-FEB-1996.
 XX
 PF 06-APR-1992; 92US-0864475.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX

P1 Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1996-139028/14.
 DR N-PSDB; AAT15946.
 XX
 PT DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.
 XX
 PS Claim 1; Fig 2A-2B; 64pp; English.
 XX
 CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 585 AA;
 XX
 Query Match 4.6%; Score 25; DB 17; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNYYIHMLFVSEMLRA 191
 Db 207 GYFRLHCTRNYYIHMLFVSEMLRA 231
 XX
 RESULT 14
 AAW73315
 ID AAW73315 standard; Protein: 585 AA.
 XX
 AC AAW73315;
 XX
 DT 08-FEB-1999 (first entry)
 XX
 DE Parathyroid hormone receptor OK-O.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX
 OS Didelphis virginiana.
 XX
 XX US5840853-A.
 FN
 XX 24-NOV-1998.
 PD
 XX
 PF 06-JUN-1995; 95US-0471494.
 XX
 PR 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 DR N-PSDB; AAV08389.
 XX
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX
 PS Claim 6; Fig 2; 63pp; English.

XX This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-O, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 585 AA;
 XX
 Query Match 4.6%; Score 25; DB 20; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNYYIHMLFVSEMLRA 191
 Db 207 GYFRLHCTRNYYIHMLFVSEMLRA 231
 XX
 RESULT 15
 ABG27219
 ID ABG27219 standard; Protein: 864 AA.
 XX
 AC ABG27219;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #27210.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 FN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS91406.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 57578; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 864 AA;

Query Match 4.1%; Score 22; DB 22; Length 864;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LGASLHVWGWLMLGSCLLARAQ 25

Db 4 LGASLHVWGWLMLGSCLLARAQ 25

Search completed: November 21, 2003, 22:34:00
Job time : 48 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:33:06 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSHVWGLMLGSL.....DDILMKPSPRMESNPDTG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1035

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	100.0	541	3	US-08-468-011A-2
2	541	100.0	541	4	US-09-236-468A-2
3	541	100.0	541	5	PCT-US95-07085-2
4	60	11.1	60	3	US-08-468-011A-9
5	60	11.1	60	3	US-08-468-011A-11
6	60	11.1	60	3	US-08-468-011A-15
7	60	11.1	60	3	US-08-468-011A-19
8	60	11.1	60	4	US-09-236-468A-9
9	60	11.1	60	4	US-09-236-468A-11
10	60	11.1	60	4	US-09-236-468A-15
11	60	11.1	60	4	US-09-236-468A-19
12	59	10.9	59	3	US-08-468-011A-23
13	59	10.9	59	4	US-09-236-468A-23
14	52	9.6	52	4	US-09-236-468A-13
15	37	6.8	37	3	US-08-468-011A-25
16	37	6.8	37	4	US-09-236-468A-25
17	37	6.8	50	3	US-08-468-011A-13
18	27	5.0	575	4	US-09-449-632-5
19	25	4.6	60	3	US-08-468-011A-20
20	25	4.6	60	4	US-09-236-468A-20
21	25	4.6	515	2	US-08-468-249A-18
22	25	4.6	585	1	US-08-142-439A-6
23	25	4.6	585	2	US-08-142-551B-125
24	25	4.6	585	2	US-08-869-477-6
25	25	4.6	585	2	US-08-468-249A-19
26	21	3.9	21	3	US-08-468-011A-21
27	21	3.9	21	4	US-09-236-468A-21

28 19 3.5 449 1 US-08-142-439A-5 Sequence 5, Appli
29 19 3.5 449 2 US-08-869-477-5 Sequence 5, Appli
30 18 3.3 536 4 US-09-449-632-2 Sequence 2, Appli
31 18 3.3 591 2 US-08-468-249A-20 Sequence 20, Appli
32 18 3.3 593 2 US-08-468-249A-21 Sequence 21, Appli
33 14 2.6 19 1 US-07-864-475A-7 Sequence 7, Appli
34 14 2.6 19 2 US-08-468-249A-7 Sequence 7, Appli
35 14 2.6 60 3 US-08-468-011A-10 Sequence 10, Appli
36 14 2.6 60 4 US-09-236-468A-10 Sequence 10, Appli
37 13 2.4 458 1 US-08-112-817C-2 Sequence 2, Appli
38 13 2.4 1324 2 US-08-811-897A-56 Sequence 56, Appli
39 13 2.4 1324 4 US-09-201-474-56 Sequence 56, Appli
40 12 2.2 445 4 US-09-414-189-1 Sequence 1, Appli
41 11 2.0 542 4 US-09-449-632-4 Sequence 4, Appli
42 10 1.8 10 3 US-08-468-011A-17 Sequence 17, Appli
43 10 1.8 10 4 US-09-236-468A-17 Sequence 17, Appli
44 10 1.8 162 1 US-08-453-956-18 Sequence 18, Appli
45 10 1.8 162 1 US-08-086-631-18 Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-2

Query Match 100.0%; Score 541; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSHVWGLMLGSLRAQSDGTTFIEQIVLVKAKYQCELNITAAQLEGE 60
|||||

Db 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEBQIVLVKAKVQCELNITAOQGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNTH 180
QY 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSVDSKQVIGCKIAV 240
Db 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSVDSKQVIGCKIAV 240
QY 241 VMFIYELATNYWILVEGLYLNHLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARAT 300
Db 241 VMFIYELATNYWILVEGLYLNHLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVFVGWHYIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFVGWHYIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWGRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 2
US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match 100.0%; Score 541; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEBQIVLVKAKVQCELNITAOQGE 60
Db 1 MAWLGLSLHVGWMLGSCLLARQLDSGTITIEBQIVLVKAKVQCELNITAOQGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNTH 180

Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLHCTRNTH 180
QY 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSVDSKQVIGCKIAV 240
Db 181 MHLFVSMRLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSVDSKQVIGCKIAV 240
QY 241 VMFIYELATNYWILVEGLYLNHLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARAT 300
Db 241 VMFIYELATNYWILVEGLYLNHLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVFVGWHYIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFVGWHYIVFVCLPHSFTGLGWEIRHCELFNFSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKQWGRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
Db 421 QAEVKQWGRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 3
PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2

```
Query Match      100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLVHWGMLGSCLLARAQLDSGTTIEBQIVLVLKAKVQCELNITAOQEGE 60
DB 1 MAWLGLSLVHWGMLGSCLLARAQLDSGTTIEBQIVLVLKAKVQCELNITAOQEGE 60
QY 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPNGTWDFMHSINKTWA 120
DB 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCPNPNGTWDFMHSINKTWA 120
QY 121 NYSDCLRFQPDISIGKQBFCELYMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
DB 121 NYSDCLRFQPDISIGKQBFCELYMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNVIH 180
QY 181 MHLFVSPMLRATSFVKDRVYVHAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
DB 181 MHLFVSPMLRATSFVKDRVYVHAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYHLNLI FVAFPSDTKYLWGFILGWGPPAAFAVAAMAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYHLNLI FVAFPSDTKYLWGFILGWGPPAAFAVAAMAVARAT 300
QY 301 LADARCWELSGADIKIYQAPILAAIGLNFILFNTVRVLATKINETNAVGHDTKQYRK 360
DB 301 LADARCWELSGADIKIYQAPILAAIGLNFILFNTVRVLATKINETNAVGHDTKQYRK 360
QY 361 LAKSTLVILVFGVHYIVFVCLPHSTFTGLGWEIRMECELFNFNSFQGFVSIYCYCNGEV 420
DB 361 LAKSTLVILVFGVHYIVFVCLPHSTFTGLGWEIRMECELFNFNSFQGFVSIYCYCNGEV 420
QY 421 QAEVKQWGRNLSVDWKTTPPCGSRRCGSLVTVTHTSSQSQVAHAHAWCLSLAKLPR 480
DB 421 QAEVKQWGRNLSVDWKTTPPCGSRRCGSLVTVTHTSSQSQVAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPOTE 540
DB 481 SPADSLTATSLYLAWSGVTSQRTASHTLSTRNKEDSGRQDDILMEKPSRMESNPOTE 540
QY 541 G 541
DB 541 G 541

RESULT 4
US-08-468-011A-9
; Sequence 9, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-11

Query Match      11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYHLNLI FVAFPSDT 273
DB 1 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYHLNLI FVAFPSDT 60

RESULT 5
US-08-468-011A-11
; Sequence 11, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-11

Query Match      11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 274 KYLWGFILGWGPFAFVAWAVARATLADARCWELSGAGIKWYQAPILAAIGLNFILF 333
Db 1 KYLWGFILGWGPFAFVAWAVARATLADARCWELSGAGIKWYQAPILAAIGLNFILF 60

RESULT 6
US-08-468-011A-15
; Sequence 15, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Steven
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-15

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 BGCNCPDGLICWPRGTGKISAVCPPIYDFNKHGVAFRHCNPNGTWDFMHSINKTW 119
Db 1 BGCNCPDGLICWPRGTGKISAVCPPIYDFNKHGVAFRHCNPNGTWDFMHSINKTW 60

RESULT 7
US-08-468-011A-19
; Sequence 19, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Steven
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,

; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-19

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 137 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSPMLRAISIFV 196
Db 1 KOEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNVIHMLFVSPMLRAISIFV 60

RESULT 8
US-09-236-468A-9
; Sequence 9, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; PRIOR FILING DATE: 1999-01-25
; PRIOR FILING DATE: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-9

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 214 IMQDDPQNSIEATSDVKSQYIGCKIAVVMFYFLATNYTWLVEGLYLNLIFFVAFPSDT 273
Db 1 IMQDDPQNSIEATSDVKSQYIGCKIAVVMFYFLATNYTWLVEGLYLNLIFFVAFPSDT 60

RESULT 9
US-09-236-468A-11
; Sequence 11, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:

APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-468A-11

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 KYLWGFILGWGFFPAFVAAMAVARATLADARCWELSGADIKWYQADPILAAIGNFIIF 333
DB 1 KYLWGFILGWGFFPAFVAAMAVARATLADARCWELSGADIKWYQADPILAAIGNFIIF 60

RESULT 10
US-09-236-468A-15
Sequence 15, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-468A-15

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 EGNCFPEWGLICWPRTGKISAVPCPPYVYDENHKGVAFRCHCPNGTWDFMHSINKTW 119
DB 1 EGNCFPEWGLICWPRTGKISAVPCPPYVYDENHKGVAFRCHCPNGTWDFMHSINKTW 60

RESULT 11
US-09-236-468A-19
Sequence 19, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-468A-19

Query Match 11.1%; Score 60; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 KQFCERLYVMYTGYSISFGSLAVAILLIIGYFRRLHCTENYHMLFVSMRLATSIFV 196
DB 1 KQFCERLYVMYTGYSISFGSLAVAILLIIGYFRRLHCTENYHMLFVSMRLATSIFV 60

RESULT 12
US-08-468-011A-23
Sequence 23, Application US/08468011A
Patent No. 6030804
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
TITLE OF INVENTION: HLTG74
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-23

Query Match 10.9%; Score 59; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 TGLGWEIRMECELFNFSPQGFVSIYCYCNGEVQAEVKQWGRWNLSDWKETPPCGS 445
DB 1 TGLGWEIRMECELFNFSPQGFVSIYCYCNGEVQAEVKQWGRWNLSDWKETPPCGS 59

RESULT 13
US-09-236-468A-23
Sequence 23, Application US/09236468A
Patent No. 6338951
GENERAL INFORMATION:
APPLICANT: Soppet et al.
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
FILE REFERENCE: PF201D1
CURRENT APPLICATION NUMBER: US/09/236,468A
CURRENT FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: 08/468,011

; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-23

Query Match 10.9%; Score 59; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 3.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 387 TGLGWEIRMHCELFNSFGQFFVSIYCYNGEYQAEVKQWGRNLSVDWKRTPPCGS 445
Db 1 TGLGWEIRMHCELFNSFGQFFVSIYCYNGEYQAEVKQWGRNLSVDWKRTPPCGS 59

RESULT 14
US-09-236-468A-13
; Sequence 13, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201DI
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-13

Query Match 9.6%; Score 52; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.3e-41;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 LNTVRVLATKIWETNAVGHDRKQYRKAKSTLVLVFGVGHYIVFVCLPHS 385
Db 1 LNTVRVLATKIWETNAVGHDRKQYRKAKSTLVLVFGVGHYIVFVCLPHS 52

RESULT 15
US-08-468-011A-25
; Sequence 25, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 AQLSDSGTITIEEQIVLVKAKVQCELNITRAQLQEGE 60
Db 1 AQLSDSGTITIEEQIVLVKAKVQCELNITRAQLQEGE 37

Search completed: November 21, 2003, 22:36:28
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:35:26 ; Search time 36 Seconds
(without alignments)

2743.463 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGLSHVWGLMLGSL.....DDILMEKPSRPMESNPDETEG 541

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 666188 seqs, 182559486 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	15	US-10-225-567A-227
2	262	48.4	550	12	US-09-826-509-565
3	216	39.9	550	15	US-10-014-162-110
4	33	6.1	546	15	US-10-014-162-109
5	27	5.0	575	12	US-10-372-095-5
6	25	4.6	515	12	US-10-267-730-18
7	25	4.6	585	12	US-10-267-730-19
8	20	3.7	20	15	US-10-225-567A-1225
9	19	3.5	353	12	US-10-017-161-696
10	19	3.5	440	12	US-09-826-509-567
11	19	3.5	440	15	US-10-225-567A-310
12	18	3.3	18	15	US-10-225-567A-1224
13	18	3.3	536	12	US-10-372-095-2
14	18	3.3	591	10	US-09-943-446-7
15	18	3.3	591	10	US-09-943-446-8

16	3.3	591	12	US-10-267-730-20	Sequence 20, Appl
17	3.3	593	10	US-09-943-446-9	Sequence 9, Appl
18	3.3	593	12	US-10-267-730-21	Sequence 21, Appl
19	3.3	593	12	US-09-826-509-563	Sequence 563, App
20	3.3	593	15	US-10-225-567A-229	Sequence 229, App
21	3.3	595	10	US-09-943-446-6	Sequence 6, Appl
22	3.3	964	12	US-10-017-161-710	Sequence 710, App
23	2.6	19	12	US-10-267-730-7	Sequence 7, Appl
24	2.4	457	15	US-09-826-509-579	Sequence 569, App
25	2.4	457	15	US-10-225-567A-469	Sequence 469, App
26	2.4	1324	10	US-09-935-371-56	Sequence 56, Appl
27	2.2	268	9	US-09-796-338A-19	Sequence 19, Appl
28	2.2	268	12	US-10-145-586-19	Sequence 19, Appl
29	2.2	268	15	US-10-282-837-19	Sequence 19, Appl
30	2.2	271	9	US-09-795-693-36	Sequence 36, Appl
31	2.2	271	15	US-10-156-239-36	Sequence 36, Appl
32	2.2	271	15	US-10-199-485-36	Sequence 36, Appl
33	2.2	466	12	US-10-241-220-78	Sequence 78, Appl
34	2.2	466	12	US-09-826-509-507	Sequence 507, App
35	2.2	466	15	US-10-225-567A-128	Sequence 128, App
36	1.1	542	12	US-10-372-095-4	Sequence 4, Appl
37	1.0	11	10	US-09-966-871-62	Sequence 62, Appl
38	1.0	11	14	US-10-039-645-62	Sequence 62, Appl
39	1.0	11	15	US-10-139-084-62	Sequence 62, Appl
40	1.0	273	15	US-10-120-604-11	Sequence 11, Appl
41	1.0	477	14	US-10-010-065-6	Sequence 6, Appl
42	1.0	477	15	US-10-225-567A-134	Sequence 134, App
43	1.0	553	15	US-10-225-567A-520	Sequence 520, App
44	1.0	10	10	US-09-966-871-67	Sequence 67, Appl
45	1.7	10	14	US-10-039-645-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-227
; Sequence 227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 67.1%; Score 363; DB 15; Length 550;
Best local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	4	LGASLHVWGLMLGSCLLARQLDSGGTTIEQIVLVKAKVQCELNITAQLOEGGNC	53
Db	4	LGASLHVWGLMLGSCLLARQLDSGGTTIEQIVLVKAKVQCELNITAQLOEGGNC	63
Qy	64	FPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRNCNPGTWDFMHSLNKTWANS	123
Db	64	FPWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRNCNPGTWDFMHSLNKTWANS	123
Qy	124	DLRFLOPDISIQKQFCERLYVMYTVGYSIFGSLAVAILIIGYFRRLHCTNYHML	183
Db	124	DCLRFLOPDISIQKQFCERLYVMYTVGYSIFGSLAVAILIIGYFRRLHCTNYHML	183

QY 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSDVKSQYIGCKIAVWF 243
 Db 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSDVKSQYIGCKIAVWF 243
 QY 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLAD 303
 Db 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAK 363
 Db 304 ARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAK 363
 QY 364 STLVVLVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAE 423
 Db 364 STLVVLVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAE 423
 QY 424 VKQMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467
 Db 424 VKQMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467

RESULT 2

US-09-826-509-565
 ; Sequence 565, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
 ; TITLE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR FILING DATE: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 565
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-565

Query Match 48.4%; Score 262; DB 12; Length 550;
 Best Local Similarity 99.6%; Pred. No. 5.9e-250; Indels 0; Gaps 0;
 Matches 462; Conservative 0; Mismatches 2;

QY 4 LGASLHVGMWMLGSLCLARAQLDSGDTITIEBQIVLVKAKVQCELNITAQ:QEGEGNC 63
 Db 4 LGASLHVGMWMLGSLCLARAQLDSGDTITIEBQIVLVKAKVQCELNITAQ:QEGEGNC 63
 QY 64 PPEWDGLICWPRGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFHSLNKTWNTYS 123
 Db 64 PPEWDGLICWPRGTGVKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFHSLNKTWNTYS 123
 QY 124 DCLRFLOPDISIGKQEPFERYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNITHML 183
 Db 124 DCLRFLOPDISIGKQEPFERYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNITHML 183
 QY 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSDVKSQYIGCKIAVWF 243
 Db 184 FVSMPLRATSI FVKDRVVAHIGVKELESIMODDPONSIEATSDVKSQYIGCKIAVWF 243
 QY 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLAD 303
 Db 244 IYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLAD 303
 QY 304 ARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAK 363

Db 304 ARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAK 363
 QY 364 STLVVLVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAE 423
 Db 364 SPLVLVLFVGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAE 423
 QY 424 VKQMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467
 Db 424 VKQMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467

RESULT 3

US-10-014-162-110
 ; Sequence 110, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 110
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-014-162-110

Query Match 39.9%; Score 216; DB 15; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.6e-204; Indels 0; Gaps 0;
 Matches 216; Conservative 0; Mismatches 0;

QY 252 YWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLADARCWELSA 311
 Db 252 YWILVEGLYLNLI FVAFPSDTKYLWGFTLIGWGPFAAFVAWAVARATLADARCWELSA 311
 QY 312 GDIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAKSTLVVLV 371
 Db 312 GDIKWYQAPILAAI GLNFIPLNTVRVLATKIWETNAVGHDTRKQYKRLAKSTLVVLV 371
 QY 372 FGWHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAEVKQMSRW 431
 Db 372 FGWHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIICYCNGEVOAEVKQMSRW 431
 QY 432 NLSVDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467
 Db 432 NLSVDWKRTPPCGSRRCGSLVLTVTHTSTSSQSQVAA 467

RESULT 4

US-10-014-162-109
 ; Sequence 109, Application US/10014162
 ; Publication No. US20030032096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 109


```
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(546)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match          6.1%; Score 33; DB 15; Length 546;
Best Local Similarity 100.0%; Pred. No. 9.3e-24; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 0;

QY 148 YTVGYSISFGSLAVALLIIGYFRLHCTRYIH 180
    |||||
DB 146 YTVGYSISFGSLAVALLIIGYFRLHCTRYIH 178
    |||||

RESULT 5
US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHr and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5

Query Match          5.0%; Score 27; DB 12; Length 575;
Best Local Similarity 100.0%; Pred. No. 8.2e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0;

QY 165 IIGYFRLHCTRYIHMHFLVFSFMLRA 191
    |||||
DB 193 IIGYFRLHCTRYIHMHFLVFSFMLRA 219
    |||||

RESULT 6
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
```

```
US-10-267-730-18

Query Match          4.6%; Score 25; DB 12; Length 515;
Best Local Similarity 100.0%; Pred. No. 7e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 167 GYFRLHCTRYIHMHFLVFSFMLRA 191
    |||||
DB 207 GYFRLHCTRYIHMHFLVFSFMLRA 231
    |||||

RESULT 7
US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match          4.6%; Score 25; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.9e-16; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 167 GYFRLHCTRYIHMHFLVFSFMLRA 191
    |||||
DB 207 GYFRLHCTRYIHMHFLVFSFMLRA 231
    |||||

RESULT 8
US-10-225-567A-1225
; Sequence 1225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1225
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1225

Query Match          3.7%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 211 ESLIMQDDPQNSIEATSVDK 230
```

```
Db 1 ESLIMQDDPNSIEATSVDK 20
|||||
RESULT 9
US-10-017-161-696
; Sequence 696, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ASURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 696
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-696

Query Match 3.5%; Score 19; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 4.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNHYHMLFVSF 187
Db 23 FRLHCTRNHYHMLFVSF 41
|||||

RESULT 10
US-09-826-509-567
; Sequence 567, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/135,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 567
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-567

Query Match 3.5%; Score 19; DB 12; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNHYHMLFVSF 187
Db 167 FRLHCTRNHYHMLFVSF 185
|||||

RESULT 11
US-10-225-567A-310
; Sequence 310, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 310
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-310

Query Match 3.5%; Score 19; DB 15; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNHYHMLFVSF 187
Db 167 FRLHCTRNHYHMLFVSF 185
|||||

RESULT 12
US-10-225-567A-1224
; Sequence 1224, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1224

Query Match 3.3%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 KAKVOCELNITAOLOEGE 60
Db 1 KAKVOCELNITAOLOEGE 18
|||||

RESULT 13
US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
```

; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match 3.3%; Score 18; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRYIHMLF 184
|||
Db 167 GYFRLHCTRYIHMLF 184

RESULT 14

US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777A1vegicus
US-09-943-446-7

Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 15

US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591

; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

Query Match 3.3%; Score 18; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||
Db 290 YFLATNYWILVEGLYLH 307

Search completed: November 21, 2003, 22:40:59
Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:31:46 ; Search time 39 Seconds
(without alignments)
3579.653 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 541

Sequence: 1 MAWLGAHLVWGMWMLGSL.....DDLWKPSPWESNPDTG 541

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- SPTREMBL.23.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mmc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertibrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	363	67.1	621	4	Q8N429	Q8N429 homo sapien
2	38	7.0	169	11	Q9R1D4	Q9R1D4 mus musculus
3	38	7.0	237	11	Q8BUN8	Q8BUN8 mus musculus
4	38	7.0	546	11	Q91V95	Q91V95 mus musculus
5	27	5.0	575	13	Q3PWB7	Q3PWB7 brachydanio
6	20	3.7	94	13	Q3PRG1	Q3PRG1 ictalurus p
7	19	3.5	528	4	Q81V17	Q81V17 homo sapien
8	18	3.3	333	4	Q8NSV1	Q8NSV1 homo sapien
9	18	3.3	536	13	Q3PVD3	Q3PVD3 brachydanio
10	18	3.3	591	11	Q91WV4	Q91WV4 mus musculus
11	18	3.3	595	6	Q9TU31	Q9TU31 canis famil
12	18	3.3	264	4	Q8NHB4	Q8NHB4 homo sapien
13	16	3.0	419	13	Q8AXV3	Q8AXV3 figu rubrip
14	13	2.4	418	13	Q3RIB2	Q3RIB2 gallus gall
15	13	2.4	444	13	Q9YHC6	Q9YHC6 rana ridibu
16	13	2.4	459	11	Q9J140	Q9J140 mus musculus

ALIGNMENTS

RESULT 1

Q8N429 ID Q8N429 PRELIMINARY; PRT; 621 AA.

AC Q8N429; DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Parathyroid hormone receptor 2 (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Srausberg R;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036811; AAH36811.1; --
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM_1
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SMO0008; HormR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
FT NON TER 1 1
SQ SEQUENCE 621 AA; 6929 MW; 8B0A5A84889436D2 CRC64;

Query Match 67.1%; Score 363; DB 4; Length 621;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHWGWMWMLGSCLLARAQLDSGTTTBEQIVLVKAKVQCELNITAIQLEGEGNC 63

Db 75 LGASLHWGWMWMLGSCLLARAQLDSGTTTBEQIVLVKAKVQCELNITAIQLEGEGNC 134

Q9PVD2 brachydanio
Q9J1Y4 mus musculus
Q9YHC8 rana ridibu
Q8WUR8 homo sapien
Q98TU4 brachydanio
Q89S55 meleagris g
Q8WNR0 ovis aries
Q8WMD9 ovis aries
Q8AXV4 figu rubrip
Q8BGA4 mus musculus
Q73769 carassius a
Q8XDB5 mus musculus
Q8BLT3 mus musculus
Q9GMD1 oryctolagus
Q8WXR5 homo sapien
Q57671 meleagris g
Q9YHC7 rana ridibu
Q8BMD2 mus musculus
Q8RM00 acinetobact
Q98UC1 ameaurus ne
Q8WML9 tupaia bela
Q8AWA1 oncorhynch
Q9BGU4 bos taurus
Q8WMD0 tupaia bela
Q8K3R2 mesocricetu
Q98UC0 ameaurus ne
Q8AWA2 oncorhynch
Q8WML8 tupaia bela
Q73768 carassius a

QY 64 FPEWDGLI CWPRGTGKISAVPCBPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWANY 123
 DB 135 FPEWDGLI CWPRGTGKISAVPCBPYIYDFNHKGVAFRHCPNGTWDPMHSLNKTWANY 194
 QY 124 DCLRFLOPDISIGKOEFCERLYWYTVGYSISFGSLAVAILIIGYFRRLHCTFNHYHML 183
 DB 195 DCLRFLOPDISIGKOEFCERLYWYTVGYSISFGSLAVAILIIGYFRRLHCTFNHYHML 254
 QY 184 FVSMFLRATSFVVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQYIGCKIAVWMP 243
 DB 255 FVSMFLRATSFVVDKRVVHAHIGVKELESIMQDDPONSTEATSVKQYIGCKIAVWMP 314
 QY 244 IYFLATNYWTLVGLYLHNLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAARATLAD 303
 DB 315 IYFLATNYWTLVGLYLHNLIFVAFPSDTKYLWGFTLIGWGPFAAFVAWAARATLAD 374
 QY 304 ARCWELSGADIKWYIQAAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 363
 DB 375 ARCWELSGADIKWYIQAAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 434
 QY 364 STLVLVLFVGHYTVFVCLPHSFTGLGWELRMHCELFNFSFQGFVSIYCYNGEVOAE 423
 DB 435 STLVLVLFVGHYTVFVCLPHSFTGLGWELRMHCELFNFSFQGFVSIYCYNGEVOAE 494
 QY 424 VKQWRSRWNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAA 467
 DB 495 VKQWRSRWNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQSOVAA 538

RESULT 2

Q9R1D4 PRELIMINARY; PRT; 169 AA.
 AC Q9R1D4:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Parathyroid hormone type-2 receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9367425; PubMed=10438471;
 RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.,
 RT "A G protein-coupled receptor from zebrafish is activated by human
 RT parathyroid hormone and not by human or teleost parathyroid hormone-
 RT related peptide. Implications for the evolutionary conservation of
 RT calcium-regulating peptide hormones.";
 RL J. Biol. Chem. 274:23035-23042 (1999).
 DR EMBL; AF132083; AAD51909.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 FT NON TER 169
 FT NON TER 169
 SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;
 Best Local Similarity 100.0%; Pred. No. 2.9e-31;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 353
 DB 66 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 103

RESULT 3

Q8BUM8 PRELIMINARY; PRT; 237 AA.
 AC Q8BUM8:
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Parathyroid hormone receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX STRAIN=C57BL/6J; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AF332077; AAK56105.1; -.
 DR EMBL; AF332077; AAK56105.1; -.
 DR EMBL; AF332077; AAK56105.1; -.
 DR MGI; MGI:2180917; Pthr2.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

ID Q8BUM8 PRELIMINARY; PRT; 237 AA.
 AC Q8BUM8:
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Parathyroid hormone receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK083278; BAC38840.1; -.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 237 AA; 26863 MW; FA35AC19C1FF5257 CRC64;
 Query Match 7.0%; Score 38; DB 11; Length 237;
 Best Local Similarity 100.0%; Pred. No. 3.9e-31;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 353
 DB 4 WIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYKRLAK 41

RESULT 4

Q91V95 PRELIMINARY; PRT; 546 AA.
 ID Q91V95:
 AC Q91V95:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Parathyroid hormone receptor.
 GN PTHR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ILS, and ISS;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikeira J.M.;
 RT "High-throughput Sequence Identification of Gene Coding Variants
 RT within Alcohol-Related QTLs.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AF332078; AAK56106.1; -.
 DR EMBL; AF332077; AAK56105.1; -.
 DR EMBL; AF332077; AAK56105.1; -.
 DR MGI; MGI:2180917; Pthr2.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

```
DR PROSITE; PS0227; G PROTEIN RECEPTOR F2_3; 1.
KW RECEPTOR; PS0261; G PROTEIN RECEPTOR F2_4; 1.
SQ SEQUENCE 546 AA; 61908 MW; 628051EF181A1DF3 CRC64;

Query Match 7.0%; Score 38; DB 11; Length 546;
Best Local Similarity 100.0%; Pred. No. 8.2e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLFLFNTVRLVATKIETNAVGH 353
DQ 313 WIYQAPILAAIGLFLFNTVRLVATKIETNAVGH 350

RESULT 5
Q9PWB7
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone type-2 receptor.
GN PTHR2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DQ 316 WIYQAPILAAIGLFLFNTVRLVATKIETNAVGH 353
DQ 313 WIYQAPILAAIGLFLFNTVRLVATKIETNAVGH 350

Query Match 3.7%; Score 20; DB 13; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 FIYFLATNYWILVEGLYLH 262
DQ 10 FIYFLATNYWILVEGLYLH 29

RESULT 7
Q8IV17
ID Q8IV17 PRELIMINARY; PRT; 528 AA.
AC Q8IV17
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to secretin receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035757; AAH35757.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 528 AA; 58944 MW; 6AFEE299E1A76BC2 CRC64;

Query Match 3.5%; Score 19; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 8.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNHYHMLFVSF 187
DQ 255 FRRLHCTRNHYHMLFVSF 273

RESULT 8
Q8NSV1
ID Q8NSV1 PRELIMINARY; PRT; 333 AA.
AC Q8NSV1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to parathyroid hormone receptor 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031578; AAH31578.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 333 AA; 37588 MW; B176DBBA5C6A68E4 CRC64;

 Query Match 3.3%; Score 18; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 245 YFLATNYWILVEGLYLH 262
 DR 290 YFLATNYWILVEGLYLH 307

 RESULT 9
 Q9PVD3 ID Q9PVD3 PRELIMINARY; PRT; 536 AA.
 AC Q9PVD3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Parathyroid hormone receptor PTHR.
 GN PTHR.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99428481; PubMed=10497171;
 RA Rubin D.A., Juppner H.;
 RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) and a novel receptor (PTH3R) that is preferentially activated by mammalian and fuguish parathyroid hormone-related peptide."
 RL J. Biol. Chem. 274:28185-28190 (1999).
 DR EMBL; AF132084; AAF01265.1; -.
 DR HSSP; Q03431; 1BL1.
 DR ZFIN; ZDB-GENE-991123-8; pthr1.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match 3.3%; Score 18; DB 13; Length 536;
 Best Local Similarity 100.0%; Pred. No. 9.9e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 167 GYFRLHCTRNTHMLF 184
 DB 167 GYFRLHCTRNTHMLF 184

 RESULT 10
 Q91WV4 ID Q91WV4 PRELIMINARY; PRT; 591 AA.
 AC Q91WV4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Parathyroid hormone receptor.
 GN PTHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013446; AAH13446.1; -.
 DR MGL; MGI:97801; Pthr.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63ESBAFED CRC64;

 Query Match 3.3%; Score 18; DB 11; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 245 YFLATNYWILVEGLYLH 262
 DB 290 YFLATNYWILVEGLYLH 307

 RESULT 11
 Q9TU31 ID Q9TU31 PRELIMINARY; PRT; 595 AA.
 AC Q9TU31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Parathyroid hormone receptor-1.
 GN PTH1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
 RT "Molecular cloning and functional characterization of the canine parathyroid hormone receptor-1 (PTH1)."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF167095; AAD55938.1; -.
 DR HSSP; Q03431; 1BL1.

CC	Tetradontoidea; Tetradontidae; Takifugu.
OK	NCBI_TaxID=31033;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Cardoso J.C.R., Power D.M., Canario A.V.M., Elgar G., Clark M.S.;
RT	"Isolation and characterisation of the VIPR/PACAP receptor gene family
RL	in Fugu rubripes.";
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AJ296144; CAC82588.1; -
KW	Receptor.
SQ	SEQUENCE 418 AA; 47607 MW; F21C006AA4E1B698 CRC64;
Query Match	
Best Local Similarity 100.0%; Score 16; DB 13; Length 419;	
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	172 LHCTRNYIHMHLPVSF 187
Db	130 LHCTRNYIHMHLPVSF 145
RESULT 14	
Q9IBG2	PRELIMINARY; PRT; 418 AA.
ID	Q9IBG2
AC	Q9IBG2;
DT	01-OCT-2000 (T-EMBLrel. 15, Created)
DT	01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE	Vasoactive intestinal peptide receptor (Fragment).
GN	CVIPR.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OK	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21218647; PubMed=11319166;
KA	Kansaku N., Shimada K., Ohkubo T., Saito N., Suzuki T., Matsuda Y.,
RA	Zadworny D.;
RT	"Molecular cloning of chicken vasoactive intestinal polypeptide
RT	receptor complementary DNA, tissue distribution and chromosomal
RT	localization.";
RL	Biol. Reprod. 64:1575-1581(2001).
DR	EMBL: AB029895; BAA95164.1; -
DR	InterPro; IPR000832; GPCR_secretin.
DR	InterPro; IPR001879; hormn_receptor.
DR	Pfam; PF00002; 7tm_2; 1.
DR	Pfam; PF00793; HRM; 1.
DR	SMART; PR00249; GPCRSECRETIN.
DR	SMART; SMO0008; Hormr; 1.
DR	PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR	PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR	PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW	Receptor.
FT	NON TER
FT	1 1
SQ	SEQUENCE 418 AA; 48191 MW; 7AE4796ADCE08FF3 CRC64;
Query Match	
Best Local Similarity 100.0%; Score 13; DB 13; Length 419;	
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	172 LHCTRNYIHMHLP 184
Db	130 LHCTRNYIHMHLP 142
RESULT 15	
Q9YHC6	PRELIMINARY; PRT; 444 AA.
ID	Q9YHC6
AC	Q9YHC6;
DT	01-MAY-1999 (T-EMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
 DE polypeptide receptor.
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99165178; PubMed=10067855;
 RA Alexandre D., Ancuar Y., Jegou S., Fournier A., Vaudry H.;
 RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
 RT cyclase-activating polypeptide receptor exhibits pharmacological and
 RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
 RT in mammals.";
 RL Endocrinology 140:1285-1293 (1999).
 DR EMBL; AF100644; AAD03602.1; -.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Ho1mr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 SQ SEQUENCE 444 AA; 50955 MW; 883B25B729314C4C CRC64;

Query Match 2.4%; Score 13; DB 13; Length 444;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNYYHMLF 184
 |||||
 Db 157 LHCTRNYYHMLF 169

Search completed: November 21, 2003, 22:35:21
 Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:21:14 ; Search time 46 Seconds
(Without alignment)
1866.763 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGASLHWGWLMLGSL.....DDILMEKPSRMESNPDTG 541

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 19Jun03.*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2907	100.0	541	AAW12695	G-protein parathyroid
2	2635	90.6	550	AAW1875	Human PTH2 seven t
3	2635	90.6	550	ABU56732	Lung cancer-associ
4	2635	90.6	550	ABP1871	Human parathyroid
5	2629	90.4	550	ABBS6386	Non-endogenous hum
6	2629	90.3	550	AAAB0560	Human PTH2 recepto
7	2513	86.4	561	ABU56731	Lung cancer-associ
8	2217.5	76.3	546	AAAB0559	Zat PTH2 receptor
9	1418.5	48.8	536	AAAY9600	Zebrafish parathyr

10	1418.5	48.8	536	21	AAAY90230	Zebrafish PTH1r re
11	1392	47.9	585	17	AAAR92276	Opussum kidney PTH
12	1392	47.9	585	20	AAAR73315	Parathyroid hormon
13	1391	47.9	585	13	AAAR27705	Opussum kidney PTH
14	1388	47.7	515	17	AAAR92275	Opussum kidney PTH
15	1388	47.7	515	20	AAAR73314	Parathyroid hormon
16	1375	47.3	515	13	AAAR27704	Parathyroid hormon
17	1345.5	46.3	595	24	ABG73825	Canine parathyroid
18	1336.5	46.0	593	22	AAAB71876	Human PTH2 seven t
19	1336.5	46.0	593	24	ABP1872	Human parathyroid
20	1331.5	45.8	591	17	AAAR92277	Rat bone PTH/PTHrP
21	1331.5	45.8	591	20	AAAR73316	Parathyroid hormon
22	1331.5	45.8	593	20	AAAR73317	Human Parathyroid
23	1330.5	45.8	593	22	ABBS6385	Non-endogenous hum
24	1323.5	45.5	591	13	AAAR27706	Rat bone PTH/PTHrP
25	1313	45.2	593	17	AAAR92278	Human kidney PTH/p
26	1307.5	45.0	542	21	AAAY96001	Zebrafish parathyr
27	1303.5	44.8	614	13	AAAR27707	Human kidney PTH/p
28	1302.5	44.8	523	21	AAAY90231	Zebrafish PTH3R re
29	1043	35.9	448	21	AAAY96986	Human tethered PTH
30	1043	35.9	450	21	AAAY96988	Human tethered PTH
31	1041	35.8	435	21	AAAY96987	Human tethered PTH
32	1038	35.7	446	21	AAAY96983	Tethered PTH-1 rec
33	1036	35.6	435	21	AAAB07529	A mutant parathyro
34	1007.5	34.7	335	21	AAAY96984	Tethered PTH-1 rec
35	1005.5	34.6	324	21	AAAY96985	Tethered PTH-1 rec
36	814	28.0	444	23	ABBY9166	Rana ridibunda VPA
37	801	27.6	449	13	AAAR30187	Secretin receptor.
38	791.5	27.2	459	23	ABBY9164	Mouse VPAC1 recept
39	785	27.0	458	16	AAAR72506	Porcine vasoactive
40	785	27.0	458	23	ABBY9165	Porcine VPAC1 rece
41	785	27.0	458	23	ABBY9167	Porcine VPAC1 rece
42	784	27.0	440	22	AAAB71877	Human SCRC seven t
43	784	27.0	440	23	ABBO8012	Protein identified
44	784	27.0	440	23	ABBS1202	Human secretin rec
45	784	27.0	440	24	ABP1812	Human secretin rec

ALIGNMENTS

RESULT 1

AAW12695

ID AAW12695 standard; Protein; 541 AA.

AC AAW12695;

XX

XX

DT 31-MAY-1997 (first entry)

XX

XX

DE G-protein parathyroid hormone receptor HLTDG74.

XX

DE G-protein parathyroid hormone receptor; HLTDG74; parathormone; PTH;

KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;

KW hyperphosphataemia; hypoparathyroidism; chronic tetany;

KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;

KW kidney stone; nephrolithiasis; therapy; diagnosis.

XX Homo sapiens.

XX

FN WO9639433-A1.

XX

PD 12-DEC-1996.

XX

XX

PF 05-JUN-1995; 95WO-US07085.

XX

XX

ER 05-JUN-1995; 95WO-US07085.

XX

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

XX

PI Li Y, Rosen CA, Ruben SM, Soppet DR;

XX WPI; 1997-043068/04.

DR N-PSDB; AAT59619.

XX Human G-protein parathyroid hormone receptor, HLTG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
XX Claim 9; Fig 1A-E; 62pp; English.
XX
XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AA159619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphatemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphatemia, kidney stone, nephrolisis.
XX
XX Sequence 541 AA;
XX
XX Query Match 100.0%; Score 2907; DB 18; Length 541;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-307;
XX Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MAWLGLSHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAQLOEGE 60
XX Db 1 MAWLGLSHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAQLOEGE 60
XX QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
XX Db 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
XX QY 121 NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX Db 121 NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX QY 181 MHLFVSEFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240
XX Db 181 MHLFVSEFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240
XX QY 241 VMFIYFLATNYWILVEGLYHLNLI FVAFPSDFKYLWGPFLLIGWGFPAFVAAWAVARAT 300
XX Db 241 VMFIYFLATNYWILVEGLYHLNLI FVAFPSDFKYLWGPFLLIGWGFPAFVAAWAVARAT 300
XX QY 301 LADARCWELSGADIKWYIQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDRKQYRK 360
XX Db 301 LADARCWELSGADIKWYIQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDRKQYRK 360
XX QY 361 LAKSTLVLVFGVHHIVFVCLPHSFTGLGWEIRMECELFNFNSFQGFVSIYCYCNGEV 420
XX Db 361 LAKSTLVLVFGVHHIVFVCLPHSFTGLGWEIRMECELFNFNSFQGFVSIYCYCNGEV 420
XX QY 421 QAEVKQWRNLSVDWKTTPCGSRRCGSVLTVTHSTSSQSOVAAHAWCLSLAKLPR 480
XX Db 421 QAEVKQWRNLSVDWKTTPCGSRRCGSVLTVTHSTSSQSOVAAHAWCLSLAKLPR 480
XX QY 481 SPADSLTATSLYLAHSGVTSQRTASHTLSTRSNKEDSGQRDDILMEKPSRPMSNPDTTE 540
XX Db 481 SPADSLTATSLYLAHSGVTSQRTASHTLSTRSNKEDSGQRDDILMEKPSRPMSNPDTTE 540
XX QY 541 G 541
XX Db 541 G 541
XX
XX RESULT 2
XX AAB71875
XX ID AAB71875 standard; Protein; 550 AA.
XX AC
XX AAB71875;
XX

DT 03-MAY-2001 (first entry)
XX Human PTR2 seven transmembrane domain.
XX
XX Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;
XX vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
XX immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
XX GPCR; liver fibrosis; respiratory disorder; infection;
XX chronic inflammatory disease; organ-specific autoimmunity;
XX graft rejection; cystic fibrosis.
XX
XX Homo sapiens.
XX OS
XX WO200109328-A1.
XX
XX 08-FEB-2001.
XX
XX 03-AUG-2000; 2000WO-US21278.
XX
XX 03-AUG-1999; 99US-0146916.
XX 29-FEB-2000; 2000US-0515781.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Hodge MR, Lloyd C, Weich NS;
XX
XX WPI; 2001-138653/14.
XX
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
XX for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX
XX Disclosure; Fig 2; 145pp; English.
XX
XX The present sequence is a human G-protein coupled receptor (GPCR) used
XX for comparison with the seven transmembrane domain of a novel GPCR
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate GPCR expression. Such diseases includes immune,
XX haematological, fibrotic, hepatic and respiratory disorders including
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,
XX graft rejection, graft versus host disease, cystic fibrosis and, in
XX particular, liver fibrosis. The GPCR polypeptides may be used as antigens
XX in the production of antibodies against GPCR and in assays to identify
XX modulators (agonists and antagonists) of GPCR expression and activity.
XX The anti-GPCR antibodies and GPCR antagonists may also be used to down
XX regulate GPCR expression and activity. The anti-GPCR antibodies may be
XX used as diagnostic agents for detecting the presence of GPCR
XX polypeptides in samples.
XX
XX Sequence 550 AA;
XX
XX Query Match 90.6%; Score 2635; DB 22; Length 550;
XX Best Local Similarity 91.4%; Pred. No. 3.3e-277;
XX Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
XX
XX QY 1 MAWLGLSHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAQLOEGE 60
XX Db 1 MAWLGLSHVWGLMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITAQLOEGE 60
XX QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
XX Db 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
XX QY 121 NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX Db 121 NYSDCLRFLQPDISIGKQEFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
XX QY 181 MHLFVSEFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240
XX Db 181 MHLFVSEFMLRATSI FVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSOYIGCKIAV 240

QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILGWGPPAAFAVAWAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILGWGPPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWYIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
DB 301 LADARCWELSGADIKWYIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYNGEV 420
DB 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
DB 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 480
QY 478 LPRSPADSLTATSLYLAWSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
DB 478 LPRSPADSLTATSLYLAWSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541

RESULT 3
ID ABUS6732 standard; Protein; 550 AA.
XX AC ABUS6732;
XX DB
DT 02-APR-2003 (first entry)
XX DE Lung cancer-associated polypeptide #325.
XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX OS Unidentified.
XX PN WO200286443-A2.
XX PD 31-OCT-2002.
XX PF 18-APR-2002; 2002WO-US12476.
XX PR 18-APR-2001; 2001US-284770P.
XX PR 10-MAY-2001; 2001US-290492P.
XX PR 09-NOV-2001; 2001US-339245P.
XX PR 13-NOV-2001; 2001US-350666P.
XX PR 29-NOV-2001; 2001US-334370P.
XX PR 12-APR-2002; 2002US-372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX PI Aziz N, Murray R;
XX DR WPI; 2003-093161/08.
XX DR N-PSDB; ABX76461.
XX PT Detecting a lung cancer-associated transcript in a cell from a patient
XX PT for treating lung cancer, by contacting a biological sample from the
XX PT patient with a polynucleotide that exhibits increased or decreased
XX PT expression in lung cancer -
XX PS Claim 27; Page 439-440; 453pp; English.
XX CC The invention relates to a method for detecting a lung cancer-associated
XX CC transcript in a cell from a patient, comprising contacting a biological
XX CC sample from the patient with a polynucleotide that selectively hybridizes

CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.
XX SQ Sequence 550 AA;
Query Match 90.6%; Score 2635; DB 24; Length 550;
Best Local Similarity 91.4%; Pred. No. 3.3e-277;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
QY 1 MAWLGLASLHVWGLMLGSCLLARALQSDGTITIERQIVLVLKAKVQCELNITAOQE 60
DB 1 MAGLGLASLHVWGLMLGSCLLARALQSDGTITIERQIVLVLKAKVQCELNITAOQE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPNGTWDFHSLNKTWA 120
DB 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPNGTWDFHSLNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQBFERLYVMYTVGVYSISFGSLAVAILIIGYFRLHCTRYIH 180
DB 121 NYSDCLRFLOPDISIGKQBFERLYVMYTVGVYSISFGSLAVAILIIGYFRLHCTRYIH 180
QY 181 MELFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPONSTEATSVDKSQYIGCKIAV 240
DB 181 MELFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPONSTEATSVDKSQYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILGWGPPAAFAVAWAVARAT 300
DB 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFFILGWGPPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWYIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
DB 301 LADARCWELSGADIKWYIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDRKQYRK 360
QY 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYNGEV 420
DB 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIYCYNGEV 420
QY 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
DB 421 QAEVKKMSRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 480
QY 478 LPRSPADSLTATSLYLAWSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
DB 478 LPRSPADSLTATSLYLAWSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
QY 535 SNPDTEG 541
DB 535 SNPDTEG 541
RESULT 4
ID ABP81871 standard; Protein; 550 AA.
XX AC ABP81871;
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 2 protein SEQ ID NO:227.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; ABZ42718.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 KW (GPCR), useful for diagnosing and designing drugs for treating
 KW conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 KW cancer or autoimmune diseases -

XX Disclosure; Fig 1; 52pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 550 AA;

XX Query Match 90.6%; Score 2635; DB 24; Length 550;

XX Best Local Similarity 91.4%; Pred. No. 3.3e-277;

XX Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

XX 1 MAMLGASLHVWGMVGLGSCILARAQLDSDGTITIEQIVLVLRKAKVQCELNITAQOEGE 60

XX 1 MAMLGASLHVWGMVGLGSCILARAQLDSDGTITIEQIVLVLRKAKVQCELNITAQOEGE 60

QY 61 GNCPPWDGLICWPRGTGKISAVPCPPYTYDNNHGVAFPHCNPNGTWDFMHLNKTWA 120
 DB 61 GNCPPWDGLICWPRGTGKISAVPCPPYTYDNNHGVAFPHCNPNGTWDFMHLNKTWA 120
 QY 121 NYSDCLEFLQPDLSIGKQPCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYYH 180
 DB 121 NYSDCLEFLQPDLSIGKQPCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNYYH 180
 QY 181 MHLFVSMFLRATSI FVKDRVHVAHIGVKELESIMODDPONSTEATSVDSKQYIGCKIAV 240
 DB 181 MHLFVSMFLRATSI FVKDRVHVAHIGVKELESIMODDPONSTEATSVDSKQYIGCKIAV 240
 QY 241 VMFYFLATNYWILVEGLYLNLI FVAFSDTKYLWGFILICWGFPAAFVAAWAVARAT 300
 DB 241 VMFYFLATNYWILVEGLYLNLI FVAFSDTKYLWGFILICWGFPAAFVAAWAVARAT 300
 QY 301 LADARCWELSAGDIKWYQAPILAAIGLAFILFNTVRLATKIWETNAVGHTRQYRK 360
 DB 301 LADARCWELSAGDIKWYQAPILAAIGLAFILFNTVRLATKIWETNAVGHTRQYRK 360
 QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYCYCNGEV 420
 DB 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYCYCNGEV 420
 QY 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTVTTHSTSSQSQVAAAHAWCL---SLAK 477
 DB 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTVTTHSTSSQSQVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
 DB 481 IASRQPDSE-----HITLFGVMSNEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 534
 QY 535 SNPDTEG 541
 DB 535 SNPDTEG 541
 RESULT 5
 ABB56386
 ID ABB56386 standard; Protein; 550 AA.
 XX
 AC ABB56386;
 XX
 DT 18-FEB-2002 (first entry)
 DE Non-endogenous human GPCR protein, SEQ ID NO: 565.
 DE
 DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2001717172-A2.
 FN
 PD 18-OCT-2001.
 XX
 PD 05-APR-2001; 2001WO-US11098.
 PF
 XX 07-APR-2000; 2000US-195747P.
 FR
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 PI
 XX WPI; 2001-648759/74.
 DR
 XX N-PSDB; AB198022.
 XX
 PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with
 XX versions of GPCRs -
 XX
 PS Claim 1; Page 367-369; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous
 CC constitutively activated versions of known GPCRs are used in the
 CC invention for the direct identification of candidate compounds as
 CC receptor agonists, inverse agonists or partial agonists. Such
 CC agonists are useful as therapeutic agents for diseases or disorders
 CC associated with GPCRs. The present sequence is a non-endogenous
 CC version of a known human GPCR.
 XX
 SQ Sequence 550 AA;

Query Match 90.4%; Score 2629; DB 22; Length 550;
 Best Local Similarity 91.2%; Pred. No. 1.5e-276;
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGLASLHWGWLMLGSCLLARALQSDGTITIEEQIVLVLKAKVQCELNITAIQOE 60
 DB 1 MAGLGLASLHWGWLMLGSCLLARALQSDGTITIEEQIVLVLKAKVQCELNITAIQOE 60
 QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFMHSLNKTWA 120
 DB 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFMHSLNKTWA 120
 QY 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
 DB 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
 QY 181 MHLFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240
 DB 181 MHLFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240
 QY 241 VMFIYFLATNYWIIWVGLYLNHLIFVAFPSDTKYLWGFILGWGPPAFVAWAARAT 300
 DB 241 VMFIYFLATNYWIIWVGLYLNHLIFVAFPSDTKYLWGFILGWGPPAFVAWAARAT 300
 QY 301 LADARCWELSGADIKWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTRKQYRK 360
 DB 301 LADARCWELSGADIKWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTRKQYRK 360
 QY 361 LAKSTIVLVLFVGVHIVFVCLPHSTGLGWEIRHCELFNSFQGFVSIYCYCNGEV 420
 DB 361 LAKSPVLVLVFGVHIVFVCLPHSTGLGWEIRHCELFNSFQGFVSIYCYCNGEV 420
 QY 421 QAEVKQWKRNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCL---SLAK 477
 DB 421 QAEVKQWKRNLVSDWKRTPPCGSRRCGSLVTTVTHSTSSQSVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
 DB 481 IASRQDPS-----HITLFGYVMSNSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
 QY 535 SNPDTEG 541
 DB 535 SNPDTEG 541

RESULT 6
 ID AAB80560
 AA B80560 standard; Protein; 550 AA.
 XX
 AC AAB80560;
 XX
 XX
 DT 26-APR-2001 (first entry)
 XX
 DE Human PTH2 receptor amino acid sequence.
 XX
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiac;
 KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;

KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 XX leukodystrophy.
 OS Homo sapiens.
 XX
 PN WO200077042-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 15-JUN-2000; 2000WO-US16776.
 XX
 XX 15-JUN-1999; 99US-0139335.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Usdin TB, Hoare SRJ;
 PI
 XX WPI; 2001-122833/13.
 DR
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 XX treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 PT
 XX Example 4; Fig I; 106pp; English.
 PS
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
 CC hypertensive, cardiac, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC headaches, diabetes and other metabolic disorders, osteoporosis,
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 550 AA;

Query Match 90.3%; Score 2626; DB 22; Length 550;
 Best Local Similarity 91.2%; Pred. No. 3.2e-276;
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGLASLHWGWLMLGSCLLARALQSDGTITIEEQIVLVLKAKVQCELNITAIQOE 60
 DB 1 MAGLGLASLHWGWLMLGSCLLARALQSDGTITIEEQIVLVLKAKVQCELNITAIQOE 60
 QY 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFMHSLNKTWA 120
 DB 61 GNCFFPFDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTDFMHSLNKTWA 120
 QY 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
 DB 121 NYSDDLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
 QY 181 MHLFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240
 DB 181 MHLFVSFMLRATSIYFKORVVAHIGVKELESIMQDDPQNSIEATSVDKSQVIGCKIAV 240
 QY 241 VMFIYFLATNYWIIWVGLYLNHLIFVAFPSDTKYLWGFILGWGPPAFVAWAARAT 300
 DB 241 VMFIYFLATNYWIIWVGLYLNHLIFVAFPSDTKYLWGFILGWGPPAFVAWAARAT 300
 QY 301 LADARCWELSGADIKWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTRKQYRK 360

```

|||||
301 LADARCWELSGDIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
361 LAKSTLVLVFVGHVYVFCVCLPHSFTGLGWEIRMHCELFNFSGFFVSIYCYCNGEV 420
361 LAKSTLVLVFVGHVYVFCVCLPHSFTGLGWEIRMHCELFNFSGFFVSIYCYCNGEV 420
421 QAEVKMWSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAK 477
421 QAEVKMWSRWNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQVAASTRMVLISGKA 480
478 LPRSPADSLFATSLYLAWSVGTGRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
481 IASGRQPS-----HITLPGVWWSRQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
535 SNPDTEG 541
535 SNPDTEG 541

```

RESULT 7
ABU56731
ID ABU56731 standard; Protein; 561 AA.
AC ABU56731;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #324.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN W0200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002W0-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR N-PSDB; ABX76460.
XX

Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer -

Claim 27; Page 439; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated

cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.

XX Sequence 561 AA;

Query Match 86.4%; Score 2513; DB 24; Length 561;
Best Local Similarity 91.2%; Pred. No. 6.5e-264;
Matches 477; Conservative 6; Mismatches 28; Indels 12; Gaps 3;
QY 25 QLDSDGTITIEQIVLVLKAKVQCELNITAOIQEGEGNCFPEWDGLICWPRGTVGKISAV 84
DB 36 QLDSDGTITIEQIVLVLKAKVQCELNITAOIQEGEGNCFPEWDGLICWPRGTVGKISAV 95
QY 85 PCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKNTWANYSDCLRFLOPDISIGKQECERL 144
DB 96 PCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKNTWANYSDCLRFLOPDISIGKQECERL 155
QY 145 YVMYTVGYSISFGSLAVAILIIGYFRRRLHCTRNYYIMHILFVSPMLRATSIFFVKDRVVHAH 204
DB 156 YVMYTVGYSISFGSLAVAILIIGYFRRRLHCTRNYYIMHILFVSPMLRATSIFFVKDRVVHAH 215
QY 205 IGKHELESIMQDDPONSIEATSVDSQYIGCKIAVVMFYIPLATNYWILVEGLYHNL 264
DB 216 IGKHELESIMQDDPONSIEATSVDSQYIGCKIAVVMFYIPLATNYWILVEGLYHNL 275
QY 265 IFVAFSDTKYLMGFTLIGNGPAAFAVAWAVARATLADARCWELSGDIKWIYQAPILA 324
DB 276 IFVAFSDTKYLMGFTLIGNGPAAFAVAWAVARATLADARCWELSGDIKWIYQAPILA 335
QY 325 AIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAESTLVLVFVGHVYVFCVCLPH 384
DB 336 AIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAESTLVLVFVGHVYVFCVCLPH 395
QY 385 SFTGLGWEIRMHCELFNFSGFFVSIYCYCNGEVQAEVKMWSRWNLSDVMKRTPPCG 444
DB 396 SFTGLGWEIRMHCELFNFSGFFVSIYCYCNGEVQAEVKMWSRWNLSDVMKRTPPCG 455
QY 445 SRRCGSLVTTVTHSTSSQVAAAHAWCL---SLAKLPRSPADSLFATSLYLAWSVGTQS 501
DB 456 SRRCGSLVTTVTHSTSSQVAASTRMVLISGKAASRQPS-----HITLPGYVWS 509
QY 502 RTASHTLS---TRSNKEDSGRQDDILMEKPSRPMESNPDTG 541
DB 510 NSRQDCLPHSFHEETKEDSGRQDDILMEKPSRPMESNPDTG 552

RESULT 8
AAB80559

ID AAB80559 standard; Protein; 546 AA.

XX AAB80559;

AC AAB80559;

XX 26-APR-2001 (first entry)

XX Rat PTH2 receptor amino acid sequence.

XX Tuberinfundibular peptide of 39 residues; TIR39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiant;
KW cytostatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;

Db 1 MGATLIVRTLGFLFCGTLTLLSFVYGLVDADDVLTKEEQIYLLFNKAKKCERAIKSKHKTSE 60
QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHNCNPNCTWDFMHSLNKTWA 120
Db 61 GSCLPWDGILCWPEGVPGKMWSTSCPEYIDFNHKGHAYRCDLNGTWELASHNNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Db 121 NYSECAKFFPHYNQNOQREVFDRLYLITVGYISLSGLSMVATVILGYFRLHCTRYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSKQSYIGCKIAV 240
Db 181 MHLFSPMLRAISIFVKDVLVYSGSALQEMERITV-EDLKSITEAPPANKTQFIGCKVAV 239
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTHYLMGFLIGMGFPAAVAAWAVARAT 300
Db 240 TLFYFLATNYWILVEGLYHNLIFVAFPSDTHYLMGFLIGMGFPAAVAAWAVARAT 299
QY 301 LADARCWELSAGDIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHOTRKOYRK 360
Db 300 LADTECDWLSAGNLKWIYQAPILTAIVVNFLLFNIIRVLTAKLRETNAAGRCDTQOYRK 359
QY 361 LAKSTLVLVVFGVHYHVFVCLPHS-FTGLGWEIRMHCELFNSFQGFVYSIYCNCGE 419
Db 360 LKSTLVLMPLFGVHYHVFVAMPYTVSGVLWQIQMHEYMLFNSVQGFVVAIYFCNCE 419
QY 420 VQAEVKKMSRWNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKKANRRRTLALDFKRAKSGNSNTSYSGPMVSHSTSVTNVTA 464

RESULT 10
AAR92276
ID AAR92276 standard; Protein; 536 AA.
XX AAR92276;
XX
XX
XX 29-AUG-2000 (first entry)
XX Zebrafish PTH1R receptor protein sequence.
XX Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;
XX parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
XX Brachydanio rerio.
XX WO200032771-A1.
XX
XX
XX 28-MAY-1999; 99WO-US11883.
XX 30-NOV-1998; 98US-0110467.
XX (JUEP/) JUEPPNER H.
XX (RUBI/) RUBIN D A.
XX Jueppner H, Rubin DA;
XX
XX WPI; 2000-412319/35.
XX N-PSDB; AAA30828.
XX

PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
PT hormone receptor 1 for treating disorders associated with receptor
PT function -
XX
XX Claim 17; Fig 2a; 11lpp; English.
XX
XX This sequence is a parathyroid hormone receptor type 1 (PTH1R)
XX receptor protein of the invention. The invention also relates to a PTH3R
XX receptor protein. Antagonists of PTH1R or PTH3R can be used for the
XX treatment of diseases associated with an increase in PTH1R or PTH3R

CC activity, respectively. The peptides are used for diagnosis or prognosis
CC of diseases and disorders associated with PTH1R or PTH3R, such as cancer.
CC The polypeptides can be used as a molecular weight markers on sodium
CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
CC peptides and polypeptides are useful to raise antibodies, including
CC monoclonal antibodies, that bind specifically to a polypeptide. The
CC peptides are useful during diagnosis of diseases and disorders in
CC mammals involving PTH1R or PTH3R receptor expression or function.
CC Mutations that affect PTH1R or PTH3R sequence and/or expression levels
CC of PTH1R or PTH3R could be diagnostic for patients with disease or
CC disorders of a developmental, physiological or neurological nature. The
CC nucleic acid molecules are valuable for chromosome identification. The
CC mapping of DNAs to chromosomes is an important first step in
CC correlating those sequences with genes associated with disease.
XX
XX Sequence 536 AA;
QY
Query Match 48.8%; Score 1418.5; DB 21; Length 536;
Best Local Similarity 57.8%; Pred. No. 7.9e-145;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;
QY 4 LGASLHV--WGWLMLGSCCL-LABAQLDSQDTITIBEQIVLVLKAKVQCELNITAOIQEGR 60
Db 1 MGATLIVRTLGFLFCGTLTLLSFVYGLVDADDVLTKEEQIYLLFNKAKKCERAIKSKHKTSE 60
QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHNCNPNCTWDFMHSLNKTWA 120
Db 61 GSCLPWDGILCWPEGVPGKMWSTSCPEYIDFNHKGHAYRCDLNGTWELASHNNKTWA 120
QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Db 121 NYSECAKFFPHYNQNOQREVFDRLYLITVGYISLSGLSMVATVILGYFRLHCTRYIH 180
QY 181 MHLFVSPMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSKQSYIGCKIAV 240
Db 181 MHLFSPMLRAISIFVKDVLVYSGSALQEMERITV-EDLKSITEAPPANKTQFIGCKVAV 239
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTHYLMGFLIGMGFPAAVAAWAVARAT 300
Db 240 TLFYFLATNYWILVEGLYHNLIFVAFPSDTHYLMGFLIGMGFPAAVAAWAVARAT 299
QY 301 LADARCWELSAGDIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHOTRKOYRK 360
Db 300 LADTECDWLSAGNLKWIYQAPILTAIVVNFLLFNIIRVLTAKLRETNAAGRCDTQOYRK 359
QY 361 LAKSTLVLVVFGVHYHVFVCLPHS-FTGLGWEIRMHCELFNSFQGFVYSIYCNCGE 419
Db 360 LKSTLVLMPLFGVHYHVFVAMPYTVSGVLWQIQMHEYMLFNSVQGFVVAIYFCNCE 419
QY 420 VQAEVKKMSRWNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKKANRRRTLALDFKRAKSGNSNTSYSGPMVSHSTSVTNVTA 464
RESULT 11
AAR92276
ID AAR92276 standard; Protein; 585 AA.
XX AAR92276;
XX
XX 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)
XX Opossum kidney PTH/PTHrP receptor.
XX Parathyroid hormone; receptor; parathormone; PTH;
XX parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX hypercalcaemia; hypocalcaemia; cancer; opossum.
XX Didelphis virginiana.
XX US594806-A.

XX PD 27-FEB-1996.
 XX PF 06-APR-1992; 92US-0864475.
 XX PR 06-APR-1992; 92US-0864475.
 XX PR 05-APR-1991; 91US-0681702.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX DR WPI; 1996-139028/14.
 XX DR N-PSDB; AAT15946.
 XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.
 XX PS Claim 1; Fig 2A-2E; 64pp; English.
 XX CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
 CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
 CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
 CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
 CC separate genes or of a laboratory artifact. The receptor induces an
 CC increase in intracellular cAMP and calcium when challenged with PTH or
 CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
 CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
 CC and hypocalcaemia to screen for (anti)agonists and to raise antibodies.
 CC Host cells expressing the receptor can be used for diagnostic
 CC measurement of PTH serum levels.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 585 AA;
 Query Match 47.9%; Score 1392; DB 17; Length 585;
 Best Local Similarity 47.8%; Pred. No. 6.9e-142;
 Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;
 QY 24 AQLSDSGTTIEEQIVLVKAKVQCELNITAILOEGE----- 60
 DB 24 ALVDDADVITKEEQIILLRNAQCEQLKEVLVPELAESAADMWMSRAKTKKPAEK 83
 QY 61 -----GNCPEWDGLICWPRGTGKISAVPCPPYTYDFNHNKGVAFR 101
 DB 84 LYPQAESEVSRSRLQDGFCLPEWDNIVCWPAGVGVKVAVPCPDYDFNHNKGRAYR 143
 QY 102 HCNPNGTWDFMHSNKTWANYSDCLRFLOPDISIGKQECERLYVWYTYGYSISFGLAV 161
 DB 144 RCDNSGSMELVPGNNRTWANYSECVKFLTNETR--EREVDFRLGMITYTYGYSISGLTAV 201
 QY 162 AILIIQYFRRLLCTRNYYHMLFVSMRLRATSIYFKDVRVVAHIGYKELESIMODDPON 221
 DB 202 AVLLIGYFRRLLCTRNYYHMLFVSMRLRATSIYFKDVRVVAHIGYKELESIMODDPON 260
 QY 222 STEATSVDSQVIGCKIAVVMFYFLATNYTWILVEGLYHNLNIFVAFSDTKYLMGFTL 281
 DB 261 FTEPPPADKAGVGCRCVAVTVFLYFLTTNYWILVEGLYHLSLIFWAFSEKKYLMGFTL 320
 QY 282 IGWFFPAAVAVAVARATLADARCWELSGADIKWYQAPILAAIGLNFILFINTVRVLA 341
 DB 321 FQGLPFAVFAVAVTVRATLANTECWLSSGNKKWIIQVPIILAAIVVNFILFINIIRVLA 380
 QY 342 TKIWEFNAYGHTRKQYRKLAETKLVILVFGVHYIVFVCLPHS--FTGLGWEIRMCHELF 400
 DB 381 TKLRETNAGCDTRQQYRKLLKSLTLVLMPLFGVHYIVFMATPYTEVSGILWQVQHYEML 440
 QY 401 FNSFQGFVFIYCYCNGEVOAEVKQWRSNLSVDWKRTPPCGSRRCGSLVLTVTTH--- 457
 DB 441 FNSFQGFVFIYCYCNGEVOAEIKKSWRNLALDFKKAIRSGS-----STYSYGPW 493

QY 458 -STSSQSYAAAHAWCLSLAKLPRSPADSLTATSLYLAWSGYTQSTASTHTLSTRNKED 516
 DB 494 VSHTSVTNVGPRGIALSLIS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLPSSGPE 550
 QY 517 SGRQRDDILM-----EKPSRPMESNPDT 539
 DB 551 PGTKDDGYLNGSLYEPVMVGEQPPPLEERET 583
 RESULT 12
 AAW73315
 ID AAW73315 standard; Protein; 585 AA.
 XX AC AAW73315;
 XX DT 08-FEB-1999 (first entry)
 XX DE Parathyroid hormone receptor OK-O.
 XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; opossum.
 XX OS Didelphis virginiana.
 XX PN US5840853-A.
 XX PD 24-NOV-1998.
 XX PF 06-JUN-1995; 95US-0471494.
 XX PR 06-APR-1992; 92US-0864475.
 XX PR 05-APR-1991; 91US-0681702.
 XX PR 06-JUN-1995; 95US-0471494.
 XX PA (GEO) GEN HOSPITAL CORP.
 XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX DR WPI; 1999-034124/03.
 XX DR N-PSDB; AAV08389.
 XX PT Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX PS Claim 6; Fig 2; 63pp; English.
 XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor
 CC OK-O, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX SQ Sequence 585 AA;
 Query Match 47.9%; Score 1392; DB 20; Length 585;
 Best Local Similarity 47.8%; Pred. No. 6.9e-142;
 Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;
 QY 24 AQLSDSGTTIEEQIVLVKAKVQCELNITAILOEGE----- 60
 DB 24 ALVDDADVITKEEQIILLRNAQCEQLKEVLVPELAESAADMWMSRAKTKKPAEK 83
 QY 61 -----GNCPEWDGLICWPRGTGKISAVPCPPYTYDFNHNKGVAFR 101
 DB 84 LYPQAESEVSRSRLQDGFCLPEWDNIVCWPAGVGVKVAVPCPDYDFNHNKGRAYR 143
 QY 102 HCNPNGTWDFMHSNKTWANYSDCLRFLOPDISIGKQECERLYVWYTYGYSISFGLAV 161
 DB 144 RCDNSGSMELVPGNNRTWANYSECVKFLTNETR--EREVDFRLGMITYTYGYSISGLTAV 201
 QY 162 AILIIQYFRRLLCTRNYYHMLFVSMRLRATSIYFKDVRVVAHIGYKELESIMODDPON 221

Db 202 AVILGFRRLHCTRYIHHLFVSMFLRAVSIFIKDAVLSGVSTDEIER-ITEBELRA 260
QY 222 SIEATSVKDSQYIGCKIAVVMFYFLATNYWILVEGLYHNLIFVAFFSDTKYLGWFI 281
Db 261 FTEPPPADKAGFVGRVAVTVFLYLTNYWILVEGLYHLSLIFWAFFSEKYLWGT 320
QY 282 IGMGPPAAFAVAAVARATLADARCWELSGDIAKWIYQAPILAAIGLNFILFNTVRVLA 341
Db 321 FGMLPAVFAVAVVTVRATLANTECMDLSSGNKKWIIQVPIAAVNVNFIINIRVLA 380
QY 342 TKIWTNAVGHDRKQVRLAKSTLVILVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKLRETNAVGCRTQQRKLLKSTLVLMPLFGVHYIVFMATPYTEVSGILMQVQMYEML 440
QY 401 FNSFOGFFVSIYCYCNGEVOAEVKKMSRWNI.SVDMKRTPPCGSRRCGSLVLTVT 457
Db 441 FNSFOGFFVSIYCYCNGEVOAEIKKMSRWNTLALDFKKARSGS-----STYSY 493
QY 458 -STSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAWSGVTSHTLSTRNKED 516
Db 494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLP 550
QY 517 SGRQRDILM-----EKSPRMESNPDT 539
Db 551 PGTKDDGYLNGSLYEPVMVGEQPPPLEBERET 583

RESULT 13
AAR27705
ID AAR27705 standard; Protein; 585 AA.
XX AAR27705;
AC AAR27705;
DT 25-MAR-2003 (updated)
DT 16-MAR-1993 (first entry)
XX Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
XX Parathyroid hormone; related protein; calcium; antagonist;
XX antibodies; hypercalcaemia.
XX Didelphis virginiana.
XX WO9217602-A1.
XX FN 15-OCT-1992.
XX PD 06-APR-1992; 92WO-US02821.
XX PF 05-APR-1991; 91US-0681702.
XX PR 06-APR-1992; 92US-0864475.
XX PR (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX Abou-saura A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
XX WPI; 1992-366271/44.
XX DR N-PSDB; AAQ29605.
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
XX Disclosure; Fig 2; 91pp; English.
XX The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
CC is identical to the OK-H clone except at the C-terminal tail as OK-O
CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
CC The difference is attributed to a single nucleotide deleted in the OK-H

CC sequence causing a frame shift and an earlier stop codon. It is not
CC known whether OK-O and OK-H represent prods. of two separate genes or
CC are a laboratory artifact. The protein may be used in a therapeutic
CC compan. to inhibit activation of PTH or PTHrP and thus reduce the
CC level of calcium in the blood. Cods. capable of competing with PTH
CC or PTHrP for binding can be identified using the protein prod. and
CC DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between a cell receptor and a
CC ligand such as in hypercalcaemia. See also AAR27704-16.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 585 AA;
Query Match 47.9%; Score 1391; DB 13; Length 585;
Best Local Similarity 47.8%; Pred. No. 8.9e-142;
Matches 274; Conservative 93; Mismatches 136; Indels 70; Gaps 10;
QY 24 AQLDSGTTTIEBOIVLVKAKVQCELNT----- 53
Db 24 ALVDDADVITKEQIILLNAQAQCEQLKEVIRVPELAESAKDMMSRSKTKKPAEK 83
QY 54 --AQLQEG-----EGNCFPEWDGLICWPRGTGKISAVPCPPYLYDNHKGVAER 101
Db 84 LYPQAESEVSDRSRLQDGFCLPEWDNIVCWPAVGKVAVPCPDYDFDNHKGRAVR 143
QY 102 HCNPGTWDPMHSLNKTWANYSDCLRFQPDISIGKQECERLYNYVTVYGISISGLAV 161
Db 144 RCDNSGSELVPGNRTWANYSECVKFLTNETR--EREVFDRLGMITYYVYGISISGLSLV 201
QY 162 ALLIGYFRRLHCTRYIHHLFVSPMLRATSFIFKDRVVAHAIHVKELESIMQDDPON 221
Db 202 AVLILGYFRRLHCTRYIHHLFVSPMLRAVSIFINDAVLSGVSTDEIER-ITEBELRA 260
QY 222 STEATSVKDSQYIGCKIAVVMFYFLATNYWILVEGLYHNLIFVAFFSDTKYLGWFI 281
Db 261 FTEPPPADKAGFVGRVAVTVFLYLTNYWILVEGLYHLSLIFWAFFSEKYLWGT 320
QY 282 IGMGPPAAFAVAAVARATLADARCWELSGDIAKWIYQAPILAAIGLNFILFNTVRVLA 341
Db 321 FGMLPAVFAVAVVTVRATLANTECMDLSSGNKKWIIQVPIAAVNVNFIINIRVLA 380
QY 342 TKIWTNAVGHDRKQVRLAKSTLVILVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKLRETNAVGCRTQQRKLLKSTLVLMPLFGVHYIVFMATPYTEVSGILMQVQMYEML 440
QY 401 FNSFOGFFVSIYCYCNGEVOAEVKKMSRWNI.SVDMKRTPPCGSRRCGSLVLTVT 457
Db 441 FNSFOGFFVSIYCYCNGEVOAEIKKMSRWNTLALDFKKARSGS-----STYSY 493
QY 458 -STSSQSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAWSGVTSHTLSTRNKED 516
Db 494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHHQLPGYVKHGSISEN-SLP 550
QY 517 SGRQRDILM-----EKSPRMESNPDT 539
Db 551 PGTKDDGYLNGSLYEPVMVGEQPPPLEBERET 583
RESULT 14
AAR92275
ID AAR92275 standard; Protein; 515 AA.
XX
XX AAR92275;
XX
XX 25-MAR-2003 (updated)
DT 18-MAY-1996 (first entry)
XX
XX Opossum kidney PTH/PTHrP receptor.
XX Parathyroid hormone; receptor; parathormone; PTH;
KW Parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW

```
KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX
OS Didelphis virginiana.
XX
PN US5494806-A.
XX
PD 27-FEB-1996.
XX
PF 06-APR-1992; 92US-0864475.
XX
PR 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
XX WPI: 1996-139028/14.
DR N-PSDB; AAT15945.
XX
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
PT
XX
XX Claim 1; Fig 1A-1B; 64pp; English.
XX
XX Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
CC separate genes or of a laboratory artifact. The receptor induces an
CC increase in intracellular cAMP and calcium when challenged with PTH or
CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
CC Host cells expressing the receptor can be used for diagnostic
CC measurement of PTH serum levels.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 515 AA;
SQ
Query Match 47.7%; Score 1388; DB 17; Length 515;
Best Local Similarity 54.6%; Pred. No. 1.5e-141;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
QY 24 AOLDSDGTTTIEEQVLVLKAKVQCELNITAOQGE----- 60
Db 24 ALVDADDVTKEEQIILLRNAQACEQRLKEVLRVPELAESAKDWMSRS AKTKKPKARK 83
QY 61 -----GNCFPENDGLICWPRGTGKISAVPCPPYIYDFNHHGVAFR 101
Db 84 LYPQAESREVS DRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHGRAVR 143
QY 102 HCNPNGTWDFMHSLNKTWANYSDCLRFLOPDISIGQCEFLRYMYTVGYISIFGSLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECVKFLTNETR--EREVFDRLGMIYTVGYISIGSLTV 201
QY 162 ATLLIGYFRRLHCTRNHYIHMHLFVSMFLRATSI FVKDRVVAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRLHCTRNHYIHMHLFVSMFLRAVSIFIKDAVLVSGVSTDEIER-ITBEELRA 260
QY 222 STEATSDVKSOYIGCKIAVMFIYFLATNYIYILVEGLYHLNLI FVAFPSDTKYLWGFTL 281
Db 261 FTEPPADKAGVGCRAVTVEFLYFLTNYIYILVEGLYHLSLI FPAFSEKKYLWGFTL 320
QY 282 IONGPAPFAVAWAVARATLADARCWELSGAGIKM YQAPILAAI GLNPIFLNTVRVLA 341
Db 321 FGWGLPAFVAVVTVRAFLANTECDLSSGNKKMI IQPILAAI VVNFILFINIRVLA 380
QY 342 TKIETNAVGHDTROKRYKLAISTVLVLVFGVHHIVFVCLPHS-FTGLGWELRHCELF 400
Db 381 TKLRETNAGRCDTROQRYKLLKSTLLVLMPLFGVHIVFVMTPTYTEVSGILWQVQHYEML 440
```

```
QY 401 FNSFGQFFVSIYCYCNGEVOAEVKKMWSRNWLSVDWKRTPPCGS 445
Db 441 FNSFGQFFVSIYCYCNGEVOAEIKKWSRWTLALDFKRKARSGS 485

RESULT 15
AAW73314
ID AAW73314 standard; Protein; 515 AA.
XX
XX AAW73314;
XX
XX 08-FEB-1999 (first entry)
XX
XX Parathyroid hormone receptor OK-H.
XX
XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX PTH-related hypercalcaemia; opossum.
XX
XX Didelphis virginiana.
XX
XX US5840853-A.
XX
XX 24-NOV-1998.
XX
XX 06-JUN-1995; 95US-0471494.
XX
XX 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
PR 06-JUN-1995; 95US-0471494.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
XX WPI: 1999-034124/03.
DR N-PSDB; AAV08388.
XX
XX Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
PT
XX
XX Claim 6; Fig 1; 63pp; English.
XX
XX This sequence represents the opossum parathyroid hormone (PTH) receptor
CC OK-H, which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX
XX Sequence 515 AA;
SQ
Query Match 47.7%; Score 1388; DB 20; Length 515;
Best Local Similarity 54.6%; Pred. No. 1.5e-141;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
QY 24 AOLDSDGTTTIEEQVLVLKAKVQCELNITAOQGE----- 60
Db 24 ALVDADDVTKEEQIILLRNAQACEQRLKEVLRVPELAESAKDWMSRS AKTKKPKARK 83
QY 61 -----GNCFPENDGLICWPRGTGKISAVPCPPYIYDFNHHGVAFR 101
Db 84 LYPQAESREVS DRSRLQDGFCLPEWDNIVCWPAGVPGKVAVPCPDYDFNHHGRAVR 143
QY 102 HCNPNGTWDFMHSLNKTWANYSDCLRFLOPDISIGQCEFLRYMYTVGYISIFGSLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECVKFLTNETR--EREVFDRLGMIYTVGYISIGSLTV 201
QY 162 ATLLIGYFRRLHCTRNHYIHMHLFVSMFLRATSI FVKDRVVAHIGVKELESIMODDPQN 221
Db 202 AVLLIGYFRRLHCTRNHYIHMHLFVSMFLRAVSIFIKDAVLVSGVSTDEIER-ITBEELRA 260
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:25:10 ; Search time 21 Seconds
(without alignments)
1090.008 Million cell updates/sec

Title: US-09-996-569-2
Perfect score: 2907
Sequence: 1 MAWLGLSHVWGMMLGSL.....DDILMKSPRPMESNPDTG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2907	100.0	541	3	US-09-468-011A-2
2	2907	100.0	541	4	US-09-236-468A-2
3	2907	100.0	541	5	PCT-US95-07085-2
4	1672.5	57.5	575	4	US-09-449-632-5
5	1418.5	48.8	536	4	US-09-449-632-2
6	1397	48.1	585	1	US-08-142-439A-6
7	1397	48.1	585	2	US-08-869-477-6
8	1392	47.9	585	2	US-08-142-551B-125
9	1392	47.9	585	2	US-08-468-249A-19
10	1388	47.7	515	2	US-08-468-249A-18
11	1331.5	45.8	591	2	US-08-468-249A-20
12	1331.5	45.8	593	2	US-08-468-249A-21
13	1290.5	44.4	542	4	US-09-449-632-4
14	801	27.6	449	1	US-08-142-439A-5
15	801	27.6	449	2	US-08-869-477-5
16	785	27.0	458	1	US-08-112-817C-2
17	773	26.6	1324	2	US-08-811-897A-56
18	773	26.6	1324	4	US-09-201-474-56
19	713.5	24.5	437	2	US-08-538-816A-2
20	713.5	24.5	437	2	US-09-076-651-2
21	713.5	24.5	437	4	US-09-208-394-2
22	704	24.2	431	2	US-08-538-816A-9
23	704	24.2	431	2	US-09-076-651-9
24	704	24.2	431	4	US-09-208-394-9
25	702.5	24.2	438	2	US-08-538-816A-1
26	702.5	24.2	438	2	US-09-076-651-1
27	702.5	24.2	438	4	US-09-208-394-1

28	696.5	24.0	448	2	US-08-811-897A-18	Sequence 18, Appl
29	696.5	24.0	448	2	US-08-855-213-18	Sequence 18, Appl
30	696.5	24.0	448	4	US-09-201-474-18	Sequence 18, Appl
31	696.5	24.0	467	2	US-08-811-897A-19	Sequence 19, Appl
32	696.5	24.0	467	2	US-08-855-213-19	Sequence 19, Appl
33	696.5	24.0	467	4	US-09-201-474-19	Sequence 19, Appl
34	689.5	23.7	525	2	US-08-811-897A-23	Sequence 23, Appl
35	689.5	23.7	525	2	US-08-855-213-23	Sequence 23, Appl
36	689.5	23.7	525	4	US-09-201-474-23	Sequence 23, Appl
37	688.5	23.7	448	2	US-08-811-897A-16	Sequence 16, Appl
38	688.5	23.7	448	2	US-08-855-213-16	Sequence 16, Appl
39	688.5	23.7	448	4	US-09-201-474-16	Sequence 16, Appl
40	688.5	23.7	485	2	US-08-811-897A-17	Sequence 17, Appl
41	688.5	23.7	485	2	US-08-855-213-17	Sequence 17, Appl
42	688.5	23.7	485	4	US-09-201-474-17	Sequence 17, Appl
43	684.5	23.5	448	2	US-08-811-897A-22	Sequence 22, Appl
44	684.5	23.5	448	2	US-08-855-213-22	Sequence 22, Appl
45	684.5	23.5	448	4	US-09-201-474-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Vi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-2

Query Match 100.0%; Score 2907; DB 3; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWLGLSHVWGMMLGSLARQLSDGTFITIEQIVLVKAKVCELNITLAQLEGE 60
|||||

Db 1 MAWLGLSLVHWGSLMGLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAIQLQEGE 60
QY 61 GNCFFPEWDGLICWPRTGTVGKISAVPCPPYIYDNNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRTGTVGKISAVPCPPYIYDNNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSDCLEFLQPDISIGKQBFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSDCLEFLQPDISIGKQBFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNTH 180
QY 181 MHLFVSFMLRATSIYFVKORVVHAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKLAV 240
Db 181 MHLFVSFMLRATSIYFVKORVVHAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKLAV 240
QY 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFIIGWGFPAAFVAWAVARAT 300
Db 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFIIGWGFPAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLAATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLAATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTVTTHSTSSQSOVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTVTTHSTSSQSOVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 2

US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match 100.0%; Score 2907; DB 4; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSLVHWGSLMGLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAIQLQEGE 60
Db 1 MAWLGLSLVHWGSLMGLGSCLLARAQLDSGTTTIEEQIVLVKAKVQCELNITAIQLQEGE 60
QY 61 GNCFFPEWDGLICWPRTGTVGKISAVPCPPYIYDNNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRTGTVGKISAVPCPPYIYDNNHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSDCLEFLQPDISIGKQBFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNTH 180

Db 121 NYSDCLEFLQPDISIGKQBFCEFLRYVMYTVGVYSISFGSLAVAILIIGYFRRLHCTRNTH 180
QY 181 MHLFVSFMLRATSIYFVKORVVHAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKLAV 240
Db 181 MHLFVSFMLRATSIYFVKORVVHAHIGVKELESIMQDDPONSIEATSVDKSQYIGCKLAV 240
QY 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFIIGWGFPAAFVAWAVARAT 300
Db 241 VMFYFLATNYWILVEGLYLNHLIFVAFPSDTKYLWGFIIGWGFPAAFVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLAATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLAATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMCHELFNSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTVTTHSTSSQSOVAAAHAHAWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDWKRTPPCGRRCGSVLTVTTHSTSSQSOVAAAHAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRNKEDSGRQDDILMEKPSRPMESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 3

PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2


```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-869-477-6

Query Match 48.1%; Score 1397; DB 2; Length 585;
Best Local Similarity 48.0%; Pred. No. 1.6e-136;
Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;

QY 24 AQLSDSGTITIEQIVLVKAKVQCELNIT----- 53
Db 24 ALVDADDVITKEEQILLRNAQCEQLKEVLVPPELAESAADMWRSKAKTKKEPKAEK 83
QY 54 --AQLQEG-----EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDNHKGVAFR 101
Db 84 LYSQAESREVSRSRLQDGFCLPEWDNIVCPAGVPGKVAVPCPDYIDFNHKGVAFR 143
QY 102 HCNPNGTWDFHSLNKTWANYSDCLRFLOPDISICKQECERLYVMYTVGVYSIFSGSLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECVKFLNTR--EREVDFRLGMIVTVGVYSISGLTIV 201
QY 162 AILLIGYFRRHLCTRNIIHMLFVSMFLRAVSIFVKDRVVAHIGVKESLIMODDPQN 221
Db 202 AVLLIGYFRRHLCTRNIIHMLFVSMFLRAVSIFIKDAVLYSGVSTDIER-ITEELRA 260
QY 222 SIATSVDSQYIGCKIAVVMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFI 281
Db 261 FTEPPPADKAGPVGCRVAVTVPELYELTNNYVILVEGLYLSLIFMAFFSEKKYLWGFTL 320
QY 282 LGWGPFAAFVAAVARATLADARCEWLSAGDIKNYQAPILAAIGLAFILFLNTVRVLA 341
Db 321 FGWGLPAVFVAVVTVRATLANTECDJSSGNKKWIIQVPIIAAIVVNFILFIIRVLA 380
QY 342 TKIMETNAVGHDTKQYRKLAESTLVLVFVGVHVIYVPCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKLRETNAGRCDTQYRKLLKSLTLVLMPLFGVHVIYVMAVTEYTVSGILLQVQVMEYWL 440
QY 401 FNSFGGFFVSIYCYCNQEVQAEVKKMSRMNLSDWKRTPPCGRRGCGSVLTWTH--- 457
Db 441 FNSFGGFFVSIYCYCNQEVQAEIKKWSRWTLALDFRKARSGS-----STYSYGP 493
QY 458 -STSSQSOVAAAHACLSIAKLPRSPADSLTATSLYLAWSGVYQRTASHTLSTENKED 516
Db 494 VSHTSVTNVGPRGGLALSLS--PRLAPGAGASANGHQLPGVYVKGHSISEN-SLPSSGPE 550
QY 517 SGRQRDDIIM-----EKPSRPMESNPT 539
Db 551 PTKDDGYLNGSLYEPVQGEQPPILLLEERET 583

RESULT 8
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
```

```
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Deane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
; US-08-142-551B-125

Query Match 47.9%; Score 1392; DB 2; Length 585;
Best Local Similarity 47.8%; Pred. No. 5.2e-136;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

QY 24 AQLSDSGTITIEQIVLVKAKVQCELNITAQLEGE----- 60
Db 24 ALVDADDVITKEEQILLRNAQCEQLKEVLVPPELAESAADMWRSKAKTKKEPKAEK 83
QY 61 -----GNCFPEWDGLICWPRGTGKISAVPCPPYIYDNHKGVAFR 101
Db 84 LYPQAESEVSRSRLQDGFCLPEWDNIVCPAGVPGKVAVPCPDYIDFNHKGVAFR 143
QY 102 HCNPNGTWDFHSLNKTWANYSDCLRFLOPDISICKQECERLYVMYTVGVYSIFSGSLAV 161
Db 144 RCDNSGSELVPGNNRTWANYSECVKFLNTR--EREVDFRLGMIVTVGVYSISGLTIV 201
QY 162 AILLIGYFRRHLCTRNIIHMLFVSMFLRAVSIFVKDRVVAHIGVKESLIMODDPQN 221
Db 202 AVLLIGYFRRHLCTRNIIHMLFVSMFLRAVSIFIKDAVLYSGVSTDIER-ITEELRA 260
QY 222 SIATSVDSQYIGCKIAVVMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFI 281
Db 261 FTEPPPADKAGPVGCRVAVTVPELYELTNNYVILVEGLYLSLIFMAFFSEKKYLWGFTL 320
```

```
QY 282 ICGGFPAAFAVAWAVARATLADARCWELSGADIKWTIQAIPILAAIGLNFILFINTVRVLA 341
Db 321 FCGGLPAFVAVVAVVTVRATLANTECDLSSGNKKWIIQVPIILAAIYVNFILFINTVRVLA 380
QY 342 TKIWETNAVGHDRKQYRKLAKTLLVLVFGVHYIVFVCLPHS-FTGLGWEIRHCELF 400
Db 381 TKURETNAGRCDTROQYRKLLKSTLVMPLFGVHYIVFVWATPYTEVSGILWQVOMHYEML 440
QY 401 FNSFOGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCGSVLTVTH--- 457
Db 441 FNSFOGFFVSIYCYCNGEVOAEIKKWSRWTLALDFKKARSGS-----STYSYGP 493
QY 458 -STSSOSOVAHAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSTASHTLSTRNKED 516
Db 494 VSHTSVTNVGPRGLALSUS--PRLAPGAGASANGHHQLPGYVKGHSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKPSRPMSNPDT 539
Db 551 PGTKDDGYLNGSLYEPWVGEOQPPILLEBERET 583

RESULT 9
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-19

Query Match 47.9%; Score 1392; DB 2; Length 585;
Best Local Similarity 47.8%; Pred. No. 5.2e-136;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;
QY 24 AQLSDGTITIEEQIVLVKAKVQCELNITAIQEGE----- 60
```

```
Db 24 ALVDADDVITKEEQIILLRNAQCEORLKEVLRVPPELAESAQWMSRGAKTCKKPAEK 83
QY 61 -----GNCFPEDWGLICWPRGTGKISAVPCPPYTYDFNHRGVAER 101
Db 84 LYPQAESEVSDRSGRLQDGLCPEDWNIWCVAGVPKVAVPCPDYDFDNHGRAYR 143
QY 102 HCNPGTWDPMESLAKNTWANYSDCURFLQPDLSIGKQECERLYVMYTVYGISISGLAV 161
Db 144 RCDNSGWSLVPNNRTWANYSECYKFLTNETR--BREVDFRLGMIYTVYGISISGLTV 201
QY 162 ALIIGYFRLHCTNYIHMLFVGFMLRATSIKVKDRVVVHAHIGVKELESIMQDDPON 221
Db 202 AVLLIGYFRLHCTNYIHMLFVGFMLRAVSIFIKDAVLVYSGVSTDEIER-ITEELRA 260
QY 222 SIATSVDSQYIGCKIAVVMFYFLATNYIWLVEGLYHLNLIIFVAFFSDTKYLMGFIL 281
Db 261 FTEPPPADKAGFVGCRAVTVFLYFLITNYIWLVEGLYHLNLIIFMAFFSEKKYLMGFIL 320
QY 282 ICGGFPAAFAVAWAVARATLADARCWELSGADIKWTIQAIPILAAIGLNFILFINTVRVLA 341
Db 321 FCGGLPAFVAVVAVVTVRATLANTECDLSSGNKKWIIQVPIILAAIYVNFILFINTVRVLA 380
QY 342 TKIWETNAVGHDRKQYRKLAKTLLVLVFGVHYIVFVCLPHS-FTGLGWEIRHCELF 400
Db 381 TKURETNAGRCDTROQYRKLLKSTLVMPLFGVHYIVFVWATPYTEVSGILWQVOMHYEML 440
QY 401 FNSFOGFFVSIYCYCNGEVOAEVKKWMSRWNLSDVMKRTPPCGSRRCGSVLTVTH--- 457
Db 441 FNSFOGFFVSIYCYCNGEVOAEIKKWSRWTLALDFKKARSGS-----STYSYGP 493
QY 458 -STSSOSOVAHAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSTASHTLSTRNKED 516
Db 494 VSHTSVTNVGPRGLALSUS--PRLAPGAGASANGHHQLPGYVKGHSISEN-SLPSSGPE 550
QY 517 SGRQRDDILM-----EKPSRPMSNPDT 539
Db 551 PGTKDDGYLNGSLYEPWVGEOQPPILLEBERET 583

RESULT 10
US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
```


;; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
;; TITLE OF INVENTION: ENCODING SAME
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,249A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/864,475
;; FILING DATE: 06-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/681,702
;; FILING DATE: 04-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fraser, Janis K.
;; REGISTRATION NUMBER: 34,819
;; REFERENCE/DOCKET NUMBER: 00786/071003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 593 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-468-249A-21

Query Match 45.8%; Score 1331.5; DB 2; Length 593;
Best Local Similarity 47.4%; Pred. No. 1.1e-129;
Matches 276; Conservative 80; Mismatches 135; Indels 91; Gaps 11;
QY 22 ARAQLSDSGTITIEQIVLVKAKVQCELNITAQIQ----- 57
DB 22 AVALVDADDVMTKBEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EKG-----CFPEWDGLICWPRGTGKISAVPCPPYIDFNHK 96
DB 82 KASGKLYPSEEDKEAPTGSRYGRFCPLPEWDHILCWLPAGPEVAVPCPDYIDFNHK 141
QY 97 GVAFRCNPNGTWDFMHSLNKTNWYSDCLRFLOPDISICKQBFCERLYVMYTVGYSISF 156
DB 142 GHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETR--EREVDFELGWIYTVGSVL 199
QY 157 GSLAVAILIGFRRLHCTRNTHMLFVSMFMRATSIYVORVVAHIGVKELES--- 213
DB 200 ASLTAVALLIAPFRRLHCTRNTHMLFSLFSLRAVSIYKDAVLYSGATLDEAERLTEE 259
QY 214 ----IMQDDPQNSIEATSDKSYIGCKIAVVMFYFLATNYWILVEGLYHNLIFVAF 269
DB 260 ELRAIAQAPPPATAAG-----YAGCRVAVTFFLYFLATNYWILVEGLYHLSLIFMAF 314
QY 270 FSDTKYLGWFGFIPAAFAVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329
DB 315 FSEKYLWGTFFGWLPAVFAVAVSVRATLANTCGNDLSSGNKKWIIQVFIASIVLN 374
QY 330 FILFLNTVRLATKIWETNAVGHDTKQYRKLAQSLTLVLVFGVHYIYFVCLPHS-FTG 388
DB 375 FILFINIVRLATKQRETNAGRCDTQYRKLLKSLVLMPLFGVHYIYFMATPYTEVSG 434
QY 389 LGWEIRMHCELFNSFGGFVSIYCYCNGEVAQVKKWWSNLSVDWKRTPPCGSRRC 448

DB 435 TLQVQVHMYEMLFNSFGGFVSIYCYCNGEVAQVKKWWSNLTALDFKRKARSSSY 494
QY 449 G-SVLTVTTHSTSSQSAHAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTQST-AS 505
DB 495 SYCPMVSHTSVINVGPRVGLG-----LPLSPRLPTATNGHPQLPGHAKPGFPL 545
QY 506 HTLSTRS-----NKEDSGQRDDILMEK 528
DB 546 ETLETPPMAAPKODGFLNGSCGLDEASGPFRPPALIQE 587
RESULT 13
US-09-449-632-4
; Sequence 4, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: zebrafish
; US-09-449-632-4
Query Match 44.4%; Score 1290.5; DB 4; Length 542;
Best Local Similarity 48.7%; Pred. No. 1.7e-125;
Matches 259; Conservative 83; Mismatches 125; Indels 65; Gaps 10;
QY 19 CLL--ARAQLSDSGTITIEQIVLVKAKVQCELNITAQIQ--EKGNCPEWDGLICWPR 75
DB 14 CVLMGARALIDSDDVITRDEQIFLLTGARSRCERTIRAQSDVVRENNCAPEWDGIIICWPT 73
QY 76 GTVGKISAVPCPPYIDFNHKGVAHRHCNPNGTWDFMHSLNKTNWYSDCLRFLOPDISI 135
DB 74 GKPNQVAVLCPEYIDFNHGYAYRHCDASGNWQVSIINRTWANYTECTTYLHTNHS- 132
QY 136 KGOEFCERLYVMYTVGYSISFGSLAVAILIGYFRRLHCTRNTHMLFVSMFMRATSIY 195
DB 133 DQEEVFERLYMYTIGYSISLAALLVAVSILCYFKRLHCTRNTHMLFVSMFMRATSIY 192
QY 196 VKORVVAHIGVKELESIMQDDPQNSIEATSDKSYIGCKIAVVMFYFLATNYWIL 255
DB 193 VKDAVLYAVTNDGELED-----GAVEQRPVVGCKAAVTLFLYLLATNHYWIL 239
QY 256 VEGLYHNLIFVAFPSDTKYLWGFILIGWGPFAAFAVAWAVARATLADARCWELSGADIK 315
DB 240 VEGLYHLSLIFNAFLSDKNCLWALTIGWIPAVFVSIWVSARVSLADTQCWDISAGNLK 299
QY 316 WIYQAPILAAIGLNIFLNTVRLATKIWETNAVGHDTKQYRKLAQSLTLVLVFGVHY 375
DB 300 WIYQVPIAAIIVNFFLNTVRLATKIWETNAVGHDTKQYRKLAQSLTLVLVFGVHY 359
QY 376 YIVFVCLPHS-FTGLGWEIRMHCELFNSFGGFVSIYCYCNGEVAQVKKWWSNLS 434
DB 360 YMLFMALPYTDVTLGLRQLRMHYEMLFNSFGGFVSIYCYCNGEVAQVKKWWSNLS 419
QY 435 VDWKR-----TPPCGSRRCGSLVTVVTHSTSSQSAHAHAWCLSLAKLPRSPADSLTA 488
DB 420 LDLKQKARVHSGCGSGYGGMM---SHTTQ----- 449
QY 489 TSLYAMSGVTQSTASHTLSTSRNKEDSGQRDDILMEKPSRPMESNPDE 540
DB 450 -SVCLSVSQA-----KGGHSLHTIGAKGSHLOHNSNL-----PGYAPQDTE 490

RESULT 14
 US-08-142-439A-5
 ; Sequence 5, Application US/08142439A
 ; Patent No. 5670360
 ; GENERAL INFORMATION:
 ; APPLICANT: Thorens, Bernard
 ; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
 ; TITLE OF INVENTION: (GLP-1)
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: No. 56703600 No. 5670360disk of No. 5670360th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/142,439A
 ; FILING DATE: 24-NOV-93
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DK 398/92
 ; FILING DATE: 25-MAR-92
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00697
 ; FILING DATE: 23-MAR-93
 ; NAME: Harrington, James J.
 ; REGISTRATION NUMBER: 38,711
 ; REFERENCE/DOCKET NUMBER: 3756.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 449 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rattus norvegicus
 ; STRAIN: Sprague-Dawley
 ; US-08-142-439A-5
 Query Match 27.6%; Score 801; DB 1; Length 449;
 Best Local Similarity 37.3%; Pred. No. 1.1e-74;
 Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;
 QY 14 LMLGCLLAQAQLDSGTTIEQIVLVKAKVQCELNITAOI-QEGEGNCPE----- 66
 DB 12 LLLRLLLLTAKA---HTVGVPRLCDVRRVLLERAAHCLQLSKKKGALGPETASGCE 67
 QY 67 --WDGLICWPRGTGKISAVPCPPYIDFNHK-GVAFRCNPNCTWDFMHSLNKTWANY 123
 DB 68 GLWDDNCSWPSAPARTVEVQCPKFLMLSNKNGSLFRNCTODG-----WSE-- 114
 QY 124 DCLRFLOPDISIG--KQEFCEB-----LVVMTVGYSISFGSLAVAILIIGVFRILH 173
 DB 115 ---TTPRDLACGVNINNSFNERRAYLLKLVMTVGYSLSLMLLVALSILCSFRLH 171
 QY 174 CTRNYHMLFVSMRLATSFVKDQVVAHGVKLESLIMQDDPQNSIEATSVDKSQY 233
 DB 172 CTRNYHMLFVSLRALSNFIKDAV-----LFGSDD-----VTYCD-AHK 212

QY 234 IGCKIAVVMFIYFLATNYWILVEGLYLNLIFFVAFFSDTKYLWGLFGFPFAFVAA 293
 DB 213 VGCKLVMIFFQYCINANYANWLVGLYLTLLAISFFSERKYLQAFVLLGWGSPAIFVAL 272
 QY 294 WAVARATLADARCWELSA-GDIKWTYQAPIIAAIGLNFILFNTVTVRLATKIWTETNAVGH 352
 DB 273 WAITRHFLENTGCMNDINANASVWVIRGPVILSILINFIFFINILMRKLRTQETRGS 332
 QY 353 DTRQYRKLAKSTVLVLFVGVHYIVFVCLPHSFTGLGWEIRMHCELPNSFQGFVSII 412
 DB 333 ET-NHYKKLAKSTLLLIPLFGIHYIVFAFSPED----AMEVQLFFELALGSPQGLVAVL 387
 QY 413 YCYCNGEYQAEVKMWSRWNLSDMKRTPPCGSRRCGSLVLTVTHTSSQSQ 464
 DB 388 YCFLNGEVQLVQKKRWQHLQ-EPLRPVAFNNSFNATNGPTHSTKASTE 438
 RESULT 15
 US-08-869-477-5
 ; Sequence 5, Application US/08869477
 ; Patent No. 5846747
 ; GENERAL INFORMATION:
 ; APPLICANT: Thorens, Bernard
 ; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
 ; TITLE OF INVENTION: (GLP-1)
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10174-6201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/869,477
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/142,439
 ; FILING DATE: 24-NOV-93
 ; APPLICATION NUMBER: DK 398/92
 ; FILING DATE: 25-MAR-92
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00697
 ; FILING DATE: 23-MAR-93
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harrington, James J.
 ; REGISTRATION NUMBER: 38,711
 ; REFERENCE/DOCKET NUMBER: 3756.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 867 0123
 ; TELEFAX: 212 867 0298
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 449 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rattus norvegicus
 ; STRAIN: Sprague-Dawley
 ; US-08-869-477-5
 Query Match 27.6%; Score 801; DB 2; Length 449;
 Best Local Similarity 37.3%; Pred. No. 1.1e-74;

```
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;
QY 14 LMLGSCILARAQSDGTTIEBQIVLVKAKVQCCELNITRAQL-QEGEGNCPE----- 66
Db 12 LLLRLLLTAA-----HTGVPPRLCDVRRVLLEERAHCLQQLSKEKGALGPETAAGCE 67
QY 67 --WDGLICWPRGVGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHSLNKTWANY 123
Db 68 GLWNNMCSPPSAPARTVEQCPRFLMLSNKNGSLFRNCTQDG-----WSE-- 114
QY 124 DCLRFLLQPDISIG---KQEFCE-----LYVMYTVGYSSISFGSLAVAILIIGYPRRLH 173
Db 115 ---TFPRDLACGVNINNSFNERRHAYLLKLVMTYTVGYSSSLAMLLVALSILCSFRLH 171
QY 174 CTRNYTHMLFVSFMLRATSFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQY 233
Db 172 CTRNYTHMLFVSFILRALSNFIKDAV-----LFSSDD-----VTYCD-AHK 212
QY 234 ICGKIADVMEIYFLATNYWILVEGLYLNHLIFVAFESDTKYLWGFILIGWGPAAAFVAA 293
Db 213 VGCKLVNIFPQYCIMANYAWLLVEGLYHTLLAISFFSERKYLQAFVLLGWGSPAIFVAL 272
QY 294 WAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNFILNTVRVLTAKIWTNAUGH 352
Db 273 WAITRHFLENTGCDINANASVWVIRGVPILSILINFIFFINILRLMRKLTQETRGS 332
QY 353 DTRKQYRKLAKTLLVLVPGVHYIVFVCLPHSFTGLGWEIRMHCBELFNSFGPFVSII 412
Db 333 ET-NHYKRLAKSTLLIPLFGIHYIVFAFSPED---AMEVOLFFELALGSPQGLVVAVL 387
QY 413 YCYCNGEVQAEYKKWMSRWNLSDWKRTPPCGSRRCGSVLTVTTHSTSSQSQ 464
Db 388 YCFLNGEVQLEVOQKRWQHLQ-EFPLRPVAFNNSFNATNGPTHSTKASTE 438
```

Search completed: November 21, 2003, 22:28:30
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:27:30 ; Search time 35 Seconds

(without alignments)
2821.848 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGAHLVWGMLMGSL.....DDLMEKPSRPMESNPDTREG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	550	15	US-10-225-567A-227
2	2629	90.4	550	12	US-09-826-509-565
3	2600	89.4	550	15	US-10-014-162-110
4	2213.5	76.1	546	15	US-10-014-162-109
5	1672.5	57.5	575	12	US-10-372-095-5
6	1418.5	48.8	536	12	US-10-372-095-2
7	1392	47.9	585	12	US-10-267-730-19
8	1388	47.7	515	12	US-10-267-730-18
9	1345.5	46.3	593	10	US-09-943-446-6
10	1336.5	46.0	593	10	US-09-943-446-9
11	1336.5	46.0	593	15	US-10-225-567A-229
12	1331.5	45.8	591	10	US-09-943-446-7
13	1331.5	45.8	591	12	US-10-267-730-20
14	1331.5	45.8	593	12	US-10-267-730-21
15	1330.5	45.8	593	12	US-09-826-509-563

16	1324	45.5	591	10	US-09-943-446-8	Sequence 8, Appli
17	1290.5	44.4	542	12	US-10-372-095-4	Sequence 4, Appli
18	962.5	33.1	964	12	US-10-017-161-710	Sequence 710, App
19	784	27.0	440	15	US-10-225-567A-310	Sequence 310, App
20	778	26.8	440	12	US-09-826-509-567	Sequence 567, App
21	773	26.6	1324	10	US-09-935-371-56	Sequence 56, Appli
22	759.5	26.1	457	15	US-10-225-567A-469	Sequence 469, App
23	753.5	25.9	457	12	US-09-826-509-579	Sequence 579, App
24	702.5	24.2	438	15	US-10-157-031-237	Sequence 237, App
25	702.5	24.2	438	15	US-10-225-567A-471	Sequence 471, App
26	702	24.1	438	11	US-09-983-000A-20	Sequence 20, Appli
27	696.5	24.0	438	12	US-09-826-509-581	Sequence 581, App
28	696.5	24.0	448	10	US-09-935-371-18	Sequence 18, Appli
29	696.5	24.0	467	10	US-09-935-371-19	Sequence 19, Appli
30	689.5	23.7	525	10	US-09-935-371-23	Sequence 23, Appli
31	689.5	23.7	525	14	US-10-044-722-3	Sequence 3, Appli
32	689.5	23.7	525	15	US-10-225-567A-231	Sequence 231, App
33	688.5	23.7	448	10	US-09-935-371-16	Sequence 16, Appli
34	688.5	23.7	485	10	US-09-935-371-17	Sequence 17, Appli
35	684.5	23.5	448	10	US-09-935-371-22	Sequence 22, Appli
36	681.5	23.4	476	10	US-09-935-371-20	Sequence 20, Appli
37	681.5	23.4	495	10	US-09-935-371-21	Sequence 21, Appli
38	679	23.4	468	12	US-09-826-509-553	Sequence 553, App
39	675	23.2	552	10	US-09-935-371-27	Sequence 27, Appli
40	674.5	23.2	553	10	US-09-935-371-25	Sequence 25, Appli
41	673.5	23.2	476	10	US-09-935-371-14	Sequence 14, Appli
42	673.5	23.2	513	10	US-09-935-371-15	Sequence 15, Appli
43	672.5	23.1	553	10	US-09-935-371-29	Sequence 29, Appli
44	670	23.0	475	10	US-09-935-371-26	Sequence 26, Appli
45	669.5	23.0	476	10	US-09-935-371-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1

```

US-10-225-567A-227
; Sequence 227, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTO
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225.567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

```

Query Match 90.6%; Score 2635; DB 15; Length 550;
Best Local Similarity 91.4%; Pred. No. 1.3e-251;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAWLGAHLVWGMLMGSLARQLSDGTITIEEQIVLVKAKVCELNITAQLOGE 60

Db 1 MAWLGAHLVWGMLMGSLARQLSDGTITIEEQIVLVKAKVCELNITAQLOGE 60

QY 61 GNCPPENDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTWDFMHSINKTWA 120

Db 61 GNCPPENDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCPNPGTWDFMHSINKTWA 120

QY 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSTSPGSLAVAILIIGYFRHLHCTRYIH 180

Db 121 NYSCLRFLOPDISIGKQECERLYVMYTVGYSTSPGSLAVAILIIGYFRHLHCTRYIH 180


```
QY 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARAT 300
|
|
|
Db 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARAT 300
|
|
|
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
|
|
|
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
|
|
|
QY 361 LAKSTLVLVLPVGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
|
|
|
Db 361 LAKSTLVLVLPVGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
|
|
|
QY 421 QAEVKKMSRWNLSDVWKETPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
|
|
|
Db 421 QAEVKKMSRWNLSDVWKETPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
|
|
|
QY 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
|
|
|
Db 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
|
|
|
QY 535 SNPDTEG 541
|
|
|
Db 535 SNPDTEG 541
|
|
|

RESULT 2
US-09-826-509-565
; Sequence 565, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 565
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-565

Query Match 90.4%; Score 2629; DB 12; Length 550;
Best Local Similarity 91.2%; Pred. No. 4.9e-251;
Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;

QY 1 MAWLGLASLHVWGLMLGSCLLARQLDSGDTTIEEQIVLVLKAKVQCELNITAGLQEGE 60
|
|
|
Db 1 MAGLGLASLHVWGLMLGSCLLARQLDSGDTTIEEQIVLVLKAKVQCELNITAGLQEGE 60
|
|
|
QY 61 GNCFFPEWDLICWPGRGTGKISAVPCPPYIYDPFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
|
|
|
Db 61 GNCFFPEWDLICWPGRGTGKISAVPCPPYIYDPFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
|
|
|
QY 121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGVYSISFGSLAVAILIIGYFRRHLHCTRNVIH 180
|
|
|
Db 121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGVYSISFGSLAVAILIIGYFRRHLHCTRNVIH 180
|
|
|
QY 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
```

```
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
QY 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARAT 300
|
|
|
Db 241 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARAT 300
|
|
|
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
|
|
|
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
|
|
|
QY 361 LAKSTLVLVLPVGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
|
|
|
Db 361 LAKSTLVLVLPVGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
|
|
|
QY 421 QAEVKKMSRWNLSDVWKETPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
|
|
|
Db 421 QAEVKKMSRWNLSDVWKETPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
|
|
|
QY 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
|
|
|
Db 478 LPRSPADSLTATSLYLAWSGVTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
|
|
|
QY 535 SNPDTEG 541
|
|
|
Db 535 SNPDTEG 541
|
|
|

RESULT 3
US-10-014-162-110
; Sequence 110, Application US/10014162
; Publication No. US20030032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-162-110

Query Match 89.4%; Score 2600; DB 15; Length 550;
Best Local Similarity 90.9%; Pred. No. 3.6e-248;
Matches 498; Conservative 6; Mismatches 30; Indels 14; Gaps 5;

QY 1 MAWLGLASLHVWGLMLGSCLLARQLDSGDTTIEEQIVLVLKAKVQCELNITAGLQEGE 60
|
|
|
Db 1 MAGLGLASLHVWGLMLGSCLLARQLDSGDTTIEEQIVLVLKAKVQCELNITAGLQEGE 60
|
|
|
QY 61 GNCFFPEWDLICWPGRGTGKISAVPCPPYIYDPFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
|
|
|
Db 61 GNCFFPEWDLICWPGRGTGKISAVPCPPYIYDPFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
|
|
|
QY 121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGVYSISFGSLAVAILIIGYFRRHLHCTRNVIH 180
|
|
|
Db 121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGVYSISFGSLAVAILIIGYFRRHLHCTRNVIH 180
|
|
|
QY 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 239
|
|
|
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
|
|
|
QY 240 VMFIYFLATNYWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARA 299
|
|
|
Db 241 VMFIYFLATN-YWILVEGLYLHNLIFVAFSDTKYLWGPFILGWGPPAAFAVAWAVARA 299
|
|
|
```

Qy 300 TLADARWELSGAGDIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYR 359
Db 300 TLADARWELSGAGDIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYR 359
Qy 360 KLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGE 419
Db 360 KLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGE 419
Qy 420 VOAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVLTTHSTSSQSQVAAAHAWCL---SLA 476
Db 420 VOAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVLTTHSTSSQSQVAAASTRWLISGKAA 479
Qy 477 KLPRSPADSLTATSLYLAMSGVTSQRTASHLTS---TRSNKEDSGRQDDILMEKPSRPM 533
Db 480 KIARQPDSD-----HITLPGVTWNSBQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 533
Qy 534 ESNPDTEG 541
Db 534 ESNPDTEG 541

RESULT 4

US-10-014-162-109
; Sequence 109, Application US/10014162
; Publication No. US2003032096A1
; GENERAL INFORMATION:
; APPLICANT: Usdin, Ted B.
; APPLICANT: Hoare, Samuel R.J.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
; FILE REFERENCE: NIH175.001C1
; CURRENT APPLICATION NUMBER: US/10/014,162
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/1677
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139335
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(546)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-014-162-109

Query Match 76.1%; Score 2213.5; DB 15; Length 546;
Best Local Similarity 76.5%; Pred. No. 6.2e-210;
Matches 416; Conservative 37; Mismatches 82; Indels 9; Gaps 4;
Qy 1 MAWLGASHVWGLMGLSCLLARQLSDGTTITIEEQIVLVKAKVQCELNITAOQEGE 60
Db 1 MPWEALPIYIGWLLILKSLVGLAQQLSDGTTITIEEQIVLVKAKVQCELNITAOQEGE 60
Qy 61 GNCPEWDGLTCWPRGTGKISAVPCPPYIYDFNHKGVAFRHCPNGTDFMHSNKTWA 120
Db 61 GNCPEWDGLTCWPRGTAGTASMPCPYIYDFNHKGVAFRHCTPNGTDFMHSNKTWA 120
Qy 121 NYSCLAPLDISIGKQECFERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 180
Db 121 NYSDC--FLOPDINIGKQEPENLYLYTVGYSISFGSLAVAILIIGYFRRLHCTRNTH 178
Qy 181 MHLFVSFMLRATSIYFKDQVTVHAIIGVKELESIMQDDPQNSIEATSVDSKSIYGCIAV 240
Db 179 LHLFVSFMLRAXSIFVXDRVAQHLGVEALQSLVMQGLQNFIGPVSVDKSIYVGCIAV 238
Qy 241 VMFYIYFLATNYIIVLVEGLYLHNLIFVAFPSDITKYLWGFIILGNGFPAAFVAAAVARAT 300
Db 239 VMFYIYFLATNYIIVLVEGLYLHNLIFVSFFSDITKYLWGFIILGNGFPAFVAAVAVARAT 298

Qy 301 LADARWELSGAGDIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYR 360
Db 299 LADTRCWELSAGD-RWYXXPILAAIGLNFILFNTVRLATKIWETNAVGHDMRKQYR 357
Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGE 420
Db 358 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGE 417
Qy 421 QAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVLTTHSTSSQSQVAAAHAWCLSLAKLPR 480
Db 418 QAEVKKTWTRWNLSDVMKRTPPCGSRRCGSLVLTTHSTSSQSQVAAAHAWCLSLAKLPR 477
Qy 481 SPA---DSLTSATSLYLAMSGVTSQRTASHLTS---TRSNKEDSGRQDDILMEKPSRPM 537
Db 478 TACQIDSHVTLPGYVWSSSEQDCQPOS---TPBETKKGHRQDDSPVGSRRPVAFTI 534
Qy 538 DTEG 541
Db 535 DTEG 538

RESULT 5

US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609 4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5

Query Match 57.5%; Score 1672.5; DB 12; Length 575;
Best Local Similarity 60.6%; Pred. No. 2.2e-156;
Matches 321; Conservative 72; Mismatches 110; Indels 27; Gaps 7;
Qy 25 QLDSGDTITIEEQIVLVKAKVQCELNITAOQEGECNCPPEWDGLICWPRGTGKISAV 84
Db 56 QAGEDGEITAEQVQMLDLAKLQCKVSSD-DPAVGVCVPEWDGLICWPGPPTLTKT 114
Qy 85 PCPPYIYDFNHKGVAFRHCPNGTDFMHSNKTWANYSDCLRFLOPDISTGKQECERL 144
Db 115 PCGYIYDFNHGAHAYRRCDNSGSSVLAEBSNKTWNYTECIK--SPEPNKRQVFFERL 172
Qy 145 YVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNTHMHLFVSFMLRATSIYFKDQVTVH 204
Db 173 HIMYTVGYAVSFSLVAIIFIGYFRRLHCTRNTHMHLFVSFMLRATSIYFKDQVTVH 232
Qy 205 IGKLESLIMQDDPQNSIEATSVDSKSIYGCIAVVMFYIYFLATNYIIVLVEGLYLHNL 264
Db 233 AGLQESDAVLM--NNFTNAVDVA PVDTSQYMGCKVTVLFIYFLATNYIIVLVEGLYLHNL 291
Qy 265 IFVAFPSDITKYLWGFIILGNGFPAAFVAAAVARATLADARWELSGAGDIKWYQAPILAA 324
Db 292 IFNAFLSDSKYLWGFIILGNGFPAFVAAAVARATLADARWELSGAGDIKWYQAPILAA 351
Qy 325 AIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIVFVCLPH 384
Db 352 AIGLNFILFNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIVFVCLPH 411
Qy 385 SFTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGEVOAEVKWMSRWNLSDVMKRTPPCG 444

Db 412 TREGWEEMRYCELFNFSGFQFFVSIYCYNGEVQTEIKKTWRNLAFLWPKGFPVWG 471
Qy 445 SRRCGLVLTTHSTSSQVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTA 504
Db 472 SNRYGSLVTLGNSSSSQSLAAG-----PQTRSTTLPSSRVRSRSGPTVSTHA 522
Qy 505 S---HTLSTRNK-----EDGRQRDDILMEK--PSRPMESNPDE 540
Db 523 TLPGVVNSDADSLPSPIDEEPEDSAKQVDDILLKESLPTSPSGLEDDE 572

RESULT 6
US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 1999-11-30
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match 48.8%; Score 1418.5; DB 12; Length 536;
Best Local Similarity 57.8%; Pred. No. 2.6e-131;
Matches 269; Conservative 80; Mismatches 107; Indels 9; Gaps 6;

Qy 4 LGASLHV--WGMLGSCIL-LARAOLDSGTITIEBQIVLVKAKVOCELNITAOLOGE 60
Db 1 MGATLIVTLGLFCGTLFSVYGLVDADDVLTKEQIYLLFNARKKERAISKHKTSE 60
Qy 61 GNCPEWDGLICWPRTGKISAVPCPIYDFNKHGVAFCNPNGTWDFMHSLNKTTWA 120
Db 61 GSCLEPMDGILCWPEGVPGKVMVTSCEPIYDFNKHGHAYRCDLNGTWELASHNKTWA 120
Qy 121 NYSDCLRFLOPDISIGKQEFCEFLRYMYTVGYSISFGSLAVAILIIGYFRRHLCTRNTH 180
Db 121 NYSECAKFFPHYNQOERFVDRLYIYTVGYSISGLSLMVAIVTLGYFRRHLCTRNTH 180
Qy 181 MHLFVSFMLRATSIYKORVVAHIGVKELESIMODDQNSIEATSVDKSOYIGCKIAV 240
Db 181 MHLFSLFMLRALSIYKVDVLYSGALQEMERITV-EDLKSITEAPPANKTQFICKVAV 239
Qy 241 VNIYFLATNYWILVEGLYLHNLIFVAFSDTKLWGPILIGWGFPAFVAAMAVARAT 300
Db 240 TLFLYFLATNYWILVEGLYLHSLIFMTFFSDRKYLWGFLLIGWGVPMFVTIWSVRAT 299
Qy 301 LADARCWELSGADIYWIQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRK 360
Db 300 LADTECDWLSAGNLKWIQOIPILTAIVNFFLFIIRVLAITKLRNAGRCDRQYRK 359
Qy 361 LAKSTLVLVPGVHYIVFVCLPHS--FTGLGWEIRMHCELFNSPQFPVSIYCYNGE 419
Db 360 LKSTLVLMPLFGVHYIVFPMAPYTEVSGVLWQIQHVEMLFNSVQGFVAILIYCFNGE 419
Qy 420 VQAEYKRWMSRWNLSDVWKRTPPCGSR--RCGSVL--TTVTHSTS 460
Db 420 VQAEIKAWNRRTLALDPKPKARSGSNTYSYGPVMSHTSVTNVTA 464

RESULT 7

US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 47.9%; Score 1392; DB 12; Length 585;
Best Local Similarity 47.8%; Pred. No. 1.3e-128;
Matches 274; Conservative 92; Mismatches 137; Indels 70; Gaps 9;

Qy 24 AQLSDSGTITIERQIVLVKAKVOCELNITAOLOGE----- 60
Db 24 ALVDADDVITKEEQIILLRNAOACEORLKBVLRVPELAESAADMWMSRSAKTKKEKPAEK 83
Qy 61 -----GNCFPEDGLICWPRTGKISAVPCPIYDFNKHGVAFCNPNGTWDFMHSLNKTTWA 101
Db 84 LYPQAESESVSDRSRLQDGFCLPEWDNIVCWPGVPGKVAVPCDFYDFNKHGRAYR 143
Qy 102 HCNPNGTWDFMHSLNKTTWANYSDCLRFLOPDISIGKQEFCEFLRYMYTVGYSISFGSLAV 161
Db 144 RCDNSGSMELVPGNNRTWANYSECVKFLTNETR--EREVDFRLGMIYTVGYSISLGLTLV 201
Qy 162 AILLIGYFRRHLCTRNTHMHLFVSFMLRATSIYKORVVAHIGVKELESIMODDQNS 221
Db 202 AVLILGYFRRHLCTRNTHMHLFVSFMLRATSIYKORVVAHIGVKELESIMODDQNS 260
Qy 222 SIEATSVDKSOYIGCKIAVVMFIYPLATNYWILVEGLYLHNLIFVAFSDTKYLWGFIL 281
Db 261 FTEPPADKAGFVGVAVTVFLPLTNYWILVEGLYLHSLIFMFAFSEKKYLWGFIL 320
Qy 282 IGWGFPAFVAAMAVARATLADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLA 341
Db 321 FGWGLPAFVAAMAVARATLANTECWDLSSGNKKWIIQVPIILAAIVNFFILFNIIRVLA 380
Qy 342 TKIWNATVAGHDTKQYRKAKSTLVLVPGVHYIVFVCLPHS--FTGLGWEIRMHCELP 400
Db 381 TKLRNAGRCDRQYRKLLKSTLVLMPLFGVHYIVFMAFYTEVSGILWQVQMHYEML 440
Qy 401 FNSFGPFPVSIYCYNGEVOAEYKRWMSRWNLSDVWKRTPPCGSRRCGSVLTTVTH--- 457
Db 441 FNSFGFPVAILIYCFNGEVOAEIKKSWRNTLALDFRKKARSGS-----STYSYGP 493
Qy 458 -STSSQSVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRTHSTLSNKED 516
Db 494 VSHTSVTVNVPGRGGLALSLS--PRLAPGAGASANGHHQLPGVVKHGSISEN-SLPSSGPE 550
Qy 517 SGRQDDILM-----EKPSRPMESNPDT 539
Db 551 PGTCKDDGYLNGSLGYEPMVGEPPLLEBERET 583

RESULT 8
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1

GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match 47.7%; Score 1388; DB 12; Length 515;
Best Local Similarity 54.6%; Pred. No. 2.6e-128;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
24 AQLDSDGTTIEEQILVLKAKVQCELNITAOIQSGE----- 60
24 ALVDADDVITKEEQIILNNAOQCEORLKEVIRVPELAESAKOMWSRSATKTKKPAEK 83
61 -----GNCPPENDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFR 101
84 LYPQAEESREVSRLQDGPCLPNDNIVCPAGVPGKVAVPCDFYDFNHHKGRVYR 143
102 HCNPNGTWDFMHSLNKNTWANYSDCLRFLQPDISIGKQECERLYVNYTVGYSSISPGSLAV 161
144 RCDNSGSEWELVPGNRTWANYSECVFLTNETR--EREVPDRGLMIYTVGYSSISGLSTV 201
162 ALLIIGYFRRHLCTNYIHMHLFVSMFRLRATSIKVKDRVVAHIGVKELESIMQDDQON 221
202 AVLILGYFRRHLCTNYIHMHLFVSMFRLRATSIKVKDRVVAHIGVKELESIMQDDQON 260
222 SIATSVDSKSOYIGCKIAVVMYIYFLATNYIYVILVEGLYHNLIFVAPPSPDKYLGWFTL 281
261 FTEPPADKAGVGVGRVAVTVFLYFTTNYIYVILVEGLYHNLIFVAPPSEKKYLGWFTL 320
282 IGWGFPAFAVAWAVARATLADARCELSAGDIKWIYQAPILAAIGLNFILFNTVRVLA 341
321 PGWGLPAVFVAWVTVRATLANTECDLSSGNKKMIQVPIAAIWNFILFINIRVLA 380
342 TKIWTNAVGHTRQYRKLAKESTLVLVLFVGHVIVFVCLPHS--FTGLGWIRHCHCLF 400
381 TKLRETNAGRCTROQYRKLLKSTLVLMPLFGLVHIVFMATPYTEVSGILMQVQHYEML 440
401 FNSFGGFVSIYCYCNGEVQAEVKKWSRNLSVDKRTTPCGS 445
441 FNSFGGFVSIYCYCNGEVQAEIKKWSRNLTALDFKKKARSGS 485

RESULT 9
US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PCI0891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170

PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 46.3%; Score 1345.5; DB 10; Length 595;
Best Local Similarity 46.5%; Pred. No. 5.1e-124;
Matches 281; Conservative 90; Mismatches 154; Indels 79; Gaps 11;
4 LGASLHVWGLMLGSCLL---ARAQLSDGTTIEEQILVLKAKVQCELNITAOIQ--- 57
1 MCAVRIAPGLALLLCCPVLSAYALVDADDVMTKEEQIFLLHRAQAQCKRLKEVLRPA 60
58 -----EGEEN-----CFPENDGLICWPR 75
61 DIMESDKWASASTSGKPKKESKGLYPESEEDKEVFTGSHRGRPCLPENDHILCWPL 120
76 GTVGKISAVPCPPYIYDFNHHKGVAPRHCNPNGTWDFMHSLNKNTWANYSDCLRPLQPDISI 135
121 GAPGEVAVPCPDYIYDFNHHKGVAYRRCDRNGSEWELVPGNRTWANYSECVFLTNETR- 179
136 KQKQECERLYVNYTVGYSSISPGSLAVALLIIGYFRRHLCTNYIHMHLFVSMFRLRATSI 195
180 -EREVPDRGLMIYTVGYSSISGLSTVLAIIAYFRRHLCTNYIHMHLFVSMFRLRATSI 238
196 VKDRVVAHIGVKELESIMQDDPQNSIATSVDSKSOYIGCKIAVVMYIYFLA 248
239 VKDAVLYSGATLDEARLTETEELRAIAQAPPPPTAA-----GYAGCRVAVTFYFLA 292
249 TNYIYVILVEGLYHNLIFVAPPSPDKYLGWFTLIGWGFPAFAVAWAVARATLADARCEW 308
293 TNYIYVILVEGLYHNLIFVAPPSEKKYLGWFTVFGWGLPAVFVAWVSVRATLANTCGWD 352
309 LSAGDIKWIYQAPILAAIGLNFILFNTVRVLA TKIWTNAVGHTRQYRKLAKESTLV 368
353 LSSGNKKMIQVPIAAIWNFILFINIRVLA TKLRETNAGRCTROQYRKLLKSTLV 412
369 VLVFGVGHVIVFVCLPHS--FTGLGWIRHCHCLPHSFGFPVSIYCYCNGEVQAEVKK 427
413 MPLFGVGHVIVFMATPYTEVSGILMQVQHYEMLFNSFGGFVSIYCYCNGEVQAEIKK 472
428 WSRNLSVDKRTTPCGSRRCGSVLITVTHSTSSQSVAAAHAWCLSLAKLPRSPADSIT 487
473 WSRWTALDFKKKARSGSSY-SYGPMTYSHTSVTVNGPRAGLGLPLSPRLPAAATTTA 531
488 ATSLYLAGSVTQSRATSHTL-----STRSKED-----SGRQRDILMEKPSRPMES 535
532 TTNGHPPIPGHT--KPGAPTLPATPPATAAPKDDGFLNGSCGLDEASAPERPPALLAQE 589
536 NPDT 539
590 EWET 593

RESULT 10
US-09-943-446-9
; Sequence 9, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PCI0891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170

; PRIOR FILING DATE: 2000-08-30
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 593
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-943-446-9

Query Match 46.0%; Score 1336.5; DB 10; Length 593;
 Best Local Similarity 47.4%; Pred. No. 3.9e-123;
 Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;
 QY 22 ARAQLSDGTTTIEQIVLVKAKVQCELNITAQQL----- 57
 DB 22 AYALVDADVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGRPRKD 81
 QY 58 -----EGEGN----- 57
 DB 82 KASGKLYPESEDEKAPTGSRYGRPCLPEDWHILCWLPGAPGEVAVVPCPDYIDFNHK 141
 QY 97 GVAFPHCNPGTMDFMHSLNKTWANYSDCLRFQPDISIGKQBFCEBLYVMTVGYISIF 156
 DB 142 GHAYRCDRNGSWELVPGHNRWTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYSVSL 199
 QY 157 GSLAVAILIIGYFRLHCTRNYYIMHLFVSMFMRATSIPIVKDRVVAHIGVKELES- 213
 DB 200 ASLTAVAILLAYFRRLHCTRNYYIMHLFSLFMRRAVSIFVKDAVLYSGATLDEAERLTEE 259
 QY 214 ----IMODDPONSIEATSDVKSQYIGCKIAVVMFIYELATNYWILVEGLYHLNLIFFVAF 269
 DB 260 ELRAIAQAPPPATAAG-----YAGCRVATFELFLATNYWILVEGLYHLNLIFFVAF 314
 QY 270 FSDTKYLWGLFLIGWFPFAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329
 DB 315 FSEKKYLWGLFTVFGWGLPAFVAVVSVRATLANTGCDLSSGNKKWIIQVPIIASIVLN 374
 QY 330 FILELNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVGVVHIVFVCLPHS-FTG 388
 DB 375 FILELNTVRVLATKRLNETNAGRCRTQOYKRLKSTLVLMLPLFGVHYVFMATPYTEVSG 434
 QY 389 LGWEIRHCELFNSFGQFFVSIYCYCNGEVQAEVKMWSRNLSVDWKRTPPCGSRRC 448
 DB 435 TLWQVQMHYEMLFNSFGQFFVAILIYCFNCEVQAEIKKSWRWTALDFKPKARSGSSSY 494
 QY 449 G-SVLTVTHTSTSSQSVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTQSR-AS 505
 DB 495 SYGPMVSHTSVTNVPVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTTPAL 545
 QY 506 HTLSTRS-----NKEDSGRQDDILMEK 528
 DB 546 ETLTTPPAMAAPKDDGFLNGSCSLDEEASGPRPPALLOE 587

RESULT 11
 US-10-225-567A-229
 ; Sequence 229, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burmer, Glenn C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 229
 ; LENGTH: 593

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-567A-229
 Query Match 46.0%; Score 1336.5; DB 15; Length 593;
 Best Local Similarity 47.4%; Pred. No. 3.9e-123;
 Matches 276; Conservative 81; Mismatches 134; Indels 91; Gaps 11;
 QY 22 ARAQLSDGTTTIEQIVLVKAKVQCELNITAQQL----- 57
 DB 22 AYALVDADVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGRPRKD 81
 QY 58 -----EGEGN----- 57
 DB 82 KASGKLYPESEDEKAPTGSRYGRPCLPEDWHILCWLPGAPGEVAVVPCPDYIDFNHK 141
 QY 97 GVAFPHCNPGTMDFMHSLNKTWANYSDCLRFQPDISIGKQBFCEBLYVMTVGYISIF 156
 DB 142 GHAYRCDRNGSWELVPGHNRWTWANYSECYKFLTNETR--EREVDFRLGMIYTVGYSVSL 199
 QY 157 GSLAVAILIIGYFRLHCTRNYYIMHLFVSMFMRATSIPIVKDRVVAHIGVKELES- 213
 DB 200 ASLTAVAILLAYFRRLHCTRNYYIMHLFSLFMRRAVSIFVKDAVLYSGATLDEAERLTEE 259
 QY 214 ----IMODDPONSIEATSDVKSQYIGCKIAVVMFIYELATNYWILVEGLYHLNLIFFVAF 269
 DB 260 ELRAIAQAPPPATAAG-----YAGCRVATFELFLATNYWILVEGLYHLNLIFFVAF 314
 QY 270 FSDTKYLWGLFLIGWFPFAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLN 329
 DB 315 FSEKKYLWGLFTVFGWGLPAFVAVVSVRATLANTGCDLSSGNKKWIIQVPIIASIVLN 374
 QY 330 FILELNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVGVVHIVFVCLPHS-FTG 388
 DB 375 FILELNTVRVLATKRLNETNAGRCRTQOYKRLKSTLVLMLPLFGVHYVFMATPYTEVSG 434
 QY 389 LGWEIRHCELFNSFGQFFVSIYCYCNGEVQAEVKMWSRNLSVDWKRTPPCGSRRC 448
 DB 435 TLWQVQMHYEMLFNSFGQFFVAILIYCFNCEVQAEIKKSWRWTALDFKPKARSGSSSY 494
 QY 449 G-SVLTVTHTSTSSQSVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTQSR-AS 505
 DB 495 SYGPMVSHTSVTNVPVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTTPAL 545
 QY 506 HTLSTRS-----NKEDSGRQDDILMEK 528
 DB 546 ETLTTPPAMAAPKDDGFLNGSCSLDEEASGPRPPALLOE 587

RESULT 12
 US-09-943-446-7
 ; Sequence 7, Application US/09943446
 ; Patent No. US20020146777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: Castleberry, Tessa A.
 ; APPLICANT: Lu, Bihong
 ; APPLICANT: Owen, Thomas A.
 ; APPLICANT: Smock, Steven L.
 ; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
 ; FILE REFERENCE: PC10891A
 ; CURRENT APPLICATION NUMBER: US/09/943,446
 ; CURRENT FILING DATE: 2001-08-30
 ; PRIOR APPLICATION NUMBER: US 60/229,170
 ; PRIOR FILING DATE: 2000-08-30
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Rattus No. US20020146777Alvegicus
 US-09-943-446-7

Query Match	45.8%	Score 131.5	DB 12	Length 591
Best Local Similarity	46.6%	Pred. No. 1.2e-122		
Matches 270	Conservative	86	Mismatches 136	
		Indels 87	Gaps 11	
QY	22	APRAQLDSGTITIEBQIVLVLKAVQCELNTRALQ		57
		270	Conservative	86
		Mismatches	136	
		Indels	87	
		Gaps	11	

```

Db 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGGN-----CFPEWDGLICWPRGTGVIKISAVPCPPYIYDNHK 96
Db 82 KASGKLYPESEEDKEAPTGSRYRGPCLPEWDHILCWPLGAPGEVAVPCPDYIYDNHK 141
QY 97 GVAFRCHNPNCTWDFHSLNKTWANYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISF 156
Db 142 GHAYRCDRNGSWELVPGHNRWTWANYSECVKFLNETR--EREVDFRLGMIYTVGYSVSL 199
QY 157 GSLAVAILIIGYFRRLHCTRNVIHMLFVSMPLRATSI FVKDRVVHAHIGVKELES--- 213
Db 200 ASLTAVAILIAYFRRLHCTRNVIHMLFVSMPLRAVSIFVKDAVLYSGATLDEAERLTEE 259
QY 214 ----IMQDDPONSIEATSVDSQYIGCKIAVVMFYFLATNYWILVEGLYLHNLIFVAF 269
Db 260 ELRAIAQAPPPATAAG-----YAGCRVATFFLYFLATNYWILVEGLYLHSLIFMAF 314
QY 270 FSDTKYLMGFTLIGWGFPAAFVAWAVARATLADARCWELSGDIKWIYQAPILAAIGLN 329
Db 315 FSEKKYLMGFTVFGWGLPAFVAVVMSVRATLANTGCDLSSGNKKWIIQVPIIASIVLN 374
QY 330 FILPLNTVRVLATKIWETNAVGHDTKQYRKLAESTLVLVFGVHYIVFVCLPHS-PTG 388
Db 375 FILFINIVRLATKQRETNAGRCDTROQYRKLLKSLVLMPLFGVHYIVFMATPYTEVSG 434
QY 389 LGWEIRMHCELPFNSFOGFFVSIICYCNGEVOAEVKMWSRNLSVDWKRTPPCGSRRC 448
Db 435 TLMQVOMHYEMLFNSFOGFFVAILIYCFCNGEVOAEIKKWSRWTALDFKPKARSGSSY 494
QY 449 G-SVLTVTHTSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVQTORT-AS 505
Db 495 SYGPMVSHTSVTNVGPRVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTAL 545
QY 506 HTLSTRS-----NKEDSGRQDDILMEK 528
Db 546 ETLETPPAMAAPKDDGFLNGSCGLDEEASGPERPALLOE 587

```

Search completed: November 21, 2003, 22:33:01

Job time : 37 secs

```

RESULT 15
US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

```

Query Match 45.8%; Score 1330.5; DB 12; Length 593;
 Best Local Similarity 47.3%; Pred. No. 1.5e-122;
 Matches 275; Conservative 81; Mismatches 135; Indels 91; Gaps 11;

```

QY 22 ARAQLDSQGTITIEQIVLVILKAKVQCELNITAIQLQ----- 57
Db 22 AYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRPASIMESDKGWTSASTSGKPRKD 81
QY 58 -----EGGN-----CFPEWDGLICWPRGTGVIKISAVPCPPYIYDNHK 96

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:26:05 ; Search time 176 Seconds
(without alignments)

2796.966 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLASLHWGMLGSL.....DDILMKPSRPWESNPDTG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
10: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
11: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
12: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
13: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
14: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
15: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
16: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
17: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
18: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
19: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
20: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
21: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
22: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
23: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
24: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
25: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
26: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
27: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
28: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
29: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2907	100.0	541	8	US-08-468-011-2

2	2907	100.0	541	25	US-09-996-569-2	Sequence 2, Appli
3	2635	90.6	550	1	PCT-US00-21278-20	Sequence 20, Appl
4	2635	90.6	550	20	US-09-631-603-20	Sequence 20, Appl
5	2635	90.6	550	24	US-09-949-004-286	Sequence 286, App
6	2635	90.6	550	27	US-10-126-052A-663	Sequence 663, App
7	2635	90.6	550	28	US-10-225-567A-227	Sequence 227, App
8	2635	90.6	550	28	US-10-295-027-526	Sequence 526, App
9	2635	90.6	550	28	US-10-295-027-851	Sequence 851, App
10	2635	90.6	550	30	US-10-404-618-86	Sequence 86, Appl
11	2629	90.4	550	33	US-09-826-509-565	Sequence 565, App
12	2600	89.4	550	26	US-10-014-162-110	Sequence 110, App
13	2586	89.0	593	32	US-60-245-228-218	Sequence 218, App
14	2586	89.0	593	32	US-60-258-272-90	Sequence 90, Appl
15	2513	86.4	561	27	US-10-126-052A-661	Sequence 661, App
16	2513	86.4	561	28	US-10-295-027-524	Sequence 524, App
17	2213.5	76.1	546	26	US-10-014-162-109	Sequence 109, App
18	2166.5	74.5	546	27	US-10-144-779-319	Sequence 319, App
19	1822	62.7	421	21	US-09-724-676-82566	Sequence 82566, A
20	1822	62.7	421	21	US-09-724-676A-82566	Sequence 82566, A
21	1672.5	57.5	575	29	US-10-372-095-5	Sequence 5, Appli
22	1493.5	51.4	387	24	US-09-949-004-360	Sequence 360, App
23	1418.5	48.8	536	29	US-10-372-095-2	Sequence 2, Appli
24	1397	48.1	585	13	US-08-935-317-6	Sequence 6, Appli
25	1392	47.9	585	1	PCT-US94-12205-136	Sequence 136, App
26	1392	47.9	585	5	US-08-171-331-14	Sequence 14, Appl
27	1392	47.9	585	8	US-08-455-919-125	Sequence 125, App
28	1392	47.9	585	8	US-08-458-075-125	Sequence 125, App
29	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
30	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
31	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
32	1392	47.9	585	15	US-09-199-874-19	Sequence 19, Appl
33	1392	47.9	585	28	US-10-267-730-19	Sequence 19, Appl
34	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
35	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
36	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
37	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
38	1388	47.7	515	15	US-09-199-874-18	Sequence 18, Appl
39	1370.5	47.1	337	32	US-60-207-317-387	Sequence 387, App
40	1370.5	47.1	337	32	US-60-229-515-1257	Sequence 1257, Ap
41	1345.5	46.3	595	24	US-09-943-446-6	Sequence 6, Appli
42	1337	46.0	553	21	US-09-724-676-81959	Sequence 81959, A
43	1337	46.0	553	21	US-09-724-676A-81959	Sequence 81959, A
44	1336.5	46.0	593	1	PCT-US00-21278-21	Sequence 21, Appl
45	1336.5	46.0	593	20	US-09-631-603-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-468-011-2
; Sequence 2, Application US/08468011
; GENERAL INFORMATION:
; APPLICANT: Sopbet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Oistein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/468,011
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-458
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 541 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-468-011-2

Query Match 100.0%; Score 2907; DB 8; Length 541;
 Best Local Similarity 100.0%; Pred. No. 2.7e-271;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMLGASLHVWGLMLGSLCLARAQLSDGTITIEEQIVLVKAKVOCELNITAOLOGE 60
 DB 1 MAMLGASLHVWGLMLGSLCLARAQLSDGTITIEEQIVLVKAKVOCELNITAOLOGE 60
 QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 DB 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMODDPONSIEATSVDSKSOYIGCKIAV 240
 DB 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMODDPONSIEATSVDSKSOYIGCKIAV 240
 QY 241 VMFYFLATNYWILVEGLYLHNLIFVAFFSDTKYLGWFLILGWGFPAAFAVAAMAVARAT 300
 DB 241 VMFYFLATNYWILVEGLYLHNLIFVAFFSDTKYLGWFLILGWGFPAAFAVAAMAVARAT 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
 DB 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIICYCNGEV 420
 DB 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIICYCNGEV 420
 QY 421 QAEVKKQWSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 DB 421 QAEVKKQWSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 QY 481 SPADSLTATSLYLAMSGVTSRTASHTLSTRNKEDSGRORDDILMEKPSRPMSNPDTTE 540
 DB 481 SPADSLTATSLYLAMSGVTSRTASHTLSTRNKEDSGRORDDILMEKPSRPMSNPDTTE 540
 QY 541 G 541
 DB 541 G 541

RESULT 2
 US-09-996-569-2
 ; Sequence 2, Application US/09996569
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet et al.
 ; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
 ; FILE REFERENCE: PF201D1
 ; CURRENT APPLICATION NUMBER: US/09/996,569
 ; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 08/468,011
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 541
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-996-569-2

Query Match 100.0%; Score 2907; DB 25; Length 541;
 Best Local Similarity 100.0%; Pred. No. 2.7e-271;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMLGASLHVWGLMLGSLCLARAQLSDGTITIEEQIVLVKAKVOCELNITAOLOGE 60
 DB 1 MAMLGASLHVWGLMLGSLCLARAQLSDGTITIEEQIVLVKAKVOCELNITAOLOGE 60
 QY 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 DB 61 GNCPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 QY 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 DB 121 NYSDCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 QY 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMODDPONSIEATSVDSKSOYIGCKIAV 240
 DB 181 MHLFVSPMLRATSI FVKDRVVHAHIGVKELESIMODDPONSIEATSVDSKSOYIGCKIAV 240
 QY 241 VMFYFLATNYWILVEGLYLHNLIFVAFFSDTKYLGWFLILGWGFPAAFAVAAMAVARAT 300
 DB 241 VMFYFLATNYWILVEGLYLHNLIFVAFFSDTKYLGWFLILGWGFPAAFAVAAMAVARAT 300
 QY 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
 DB 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIICYCNGEV 420
 DB 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSFQGFVSIICYCNGEV 420
 QY 421 QAEVKKQWSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 DB 421 QAEVKKQWSRWNLSDVWKRTPPCGSRRRCGSLVTTVTHSTSSQSVAAAHAWCLSLAKLPR 480
 QY 481 SPADSLTATSLYLAMSGVTSRTASHTLSTRNKEDSGRORDDILMEKPSRPMSNPDTTE 540
 DB 481 SPADSLTATSLYLAMSGVTSRTASHTLSTRNKEDSGRORDDILMEKPSRPMSNPDTTE 540
 QY 541 G 541
 DB 541 G 541

RESULT 3
 PCT-US00-21278-20
 ; Sequence 20, Application PC/TUS0021278
 ; GENERAL INFORMATION:
 ; APPLICANT: Hodge, Martin R.
 ; APPLICANT: Lloyd, Clare
 ; APPLICANT: Weich, Nadine
 ; TITLE OF INVENTION: 15571, A Novel GPCR-like Molecule of the
 ; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
 ; FILE REFERENCE: 5800-48A
 ; CURRENT APPLICATION NUMBER: PCT/US00/21278
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/515,781
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/146,916
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 3.0

Db 1 MAGLGASLHVWMLGSCLLARQLDSGDTTIEEQIVLVKAKVQCELNITAOQE 60
Qy 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSNKTWA 120
Db 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSNKTWA 120
Qy 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Qy 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSQYIGCKIAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSQYIGCKIAV 240
Qy 241 VMFYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFLILGWGPPAAFAVAWAVARAT 300
Db 241 VMFYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFLILGWGPPAAFAVAWAVARAT 300
Qy 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Qy 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Qy 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Db 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Qy 478 LPRSPADSLTATSLYIAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
Db 481 IASRQPDSD---HITLPGYVWSNEQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
Qy 535 SNPDTEG 541
Db 535 SNPDTEG 541

RESULT 6
US-10-126-052A-663
; Sequence 663, Application US/10126052A
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Murray, Richard
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
; FILE REFERENCE: 018501-001530US
; CURRENT APPLICATION NUMBER: US/10/126,052A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/284,770
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/290,492
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/339,245
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,370
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 663
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-052A-663

Query Match 90.6%; Score 2635; DB 27; Length 550;

Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
Qy 1 MAGLGASLHVWMLGSCLLARQLDSGDTTIEEQIVLVKAKVQCELNITAOQE 60
Db 1 MAGLGASLHVWMLGSCLLARQLDSGDTTIEEQIVLVKAKVQCELNITAOQE 60
Qy 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSNKTWA 120
Db 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSNKTWA 120
Qy 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Db 121 NYSCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
Qy 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSQYIGCKIAV 240
Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMQDDPONSIEATSVDSQYIGCKIAV 240
Qy 241 VMFYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFLILGWGPPAAFAVAWAVARAT 300
Db 241 VMFYFLATNYWILVEGLYLNLI FVAFPSDTKYLWGFLILGWGPPAAFAVAWAVARAT 300
Qy 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDTKQYRK 360
Qy 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFSFGQFFVSIYCYCNGEV 420
Qy 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Db 421 QAEVKQWNRWNLSDVWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCL---SLAK 477
Qy 478 LPRSPADSLTATSLYIAMSGVTQSRASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
Db 481 IASRQPDSD---HITLPGYVWSNEQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
Qy 535 SNPDTEG 541
Db 535 SNPDTEG 541

RESULT 7
US-10-225-567A-227
; Sequence 227, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-227

Query Match 90.6%; Score 2635; DB 28; Length 550;

Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
Qy 1 MAGLGASLHVWMLGSCLLARQLDSGDTTIEEQIVLVKAKVQCELNITAOQE 60
Db 1 MAGLGASLHVWMLGSCLLARQLDSGDTTIEEQIVLVKAKVQCELNITAOQE 60

QY 61 GNCPEWDGLICWPRGTGCKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
 Db 61 GNCPEWDGLICWPRGTGCKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
 QY 121 NYSCLRLFLQPDISIGKQFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 Db 121 NYSCLRLFLQPDISIGKQFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 QY 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPONSIEATSVKSYIGCKIAV 240
 Db 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPONSIEATSVKSYIGCKIAV 240
 QY 241 VMFYFLATNYMILVEGLYLHNLIFVAFPSDTKYLWGFIILGWGFPFAFVAWAVARAT 300
 Db 241 VMFYFLATNYMILVEGLYLHNLIFVAFPSDTKYLWGFIILGWGFPFAFVAWAVARAT 300
 QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVILVFGVHYIVFVCLPHSFGLGWEIRMHCELFNSFGQFFVSIICYCNGEV 420
 Db 361 LAKSTLVILVFGVHYIVFVCLPHSFGLGWEIRMHCELFNSFGQFFVSIICYCNGEV 420
 QY 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVLTTHSTSSQSVAAAHAWCL---SLAK 477
 Db 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVLTTHSTSSQSVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
 Db 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
 QY 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 8

US-10-295-027-526
 ; Sequence 526, Application US/10295027
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 ; FILE REFERENCE: 018501-012500US
 ; CURRENT APPLICATION NUMBER: US/10/295,027
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 09/663,733
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/350,666
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/335,394
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: US 60/332,464
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/334,393
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: US 60/340,376
 ; PRIOR FILING DATE: 2001-12-14
 ; PRIOR APPLICATION NUMBER: US 60/347,211
 ; PRIOR FILING DATE: 2002-01-08
 ; PRIOR APPLICATION NUMBER: US 60/347,349
 ; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: US 60/356,714
 ; PRIOR FILING DATE: 2002-02-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1386
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 526
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-295-027-526

Query Match 90.6%; Score 2635; DB 28; Length 550;
 Best Local Similarity 91.4%; Pred. No. 5,7e-245;
 Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;
 QY 1 MAMGLASLHVGMMLGSCLLARAQLDSGTTIIEQIVLVLKAKVQCELNITAIQLOE 60
 Db 1 MAMGLASLHVGMMLGSCLLARAQLDSGTTIIEQIVLVLKAKVQCELNITAIQLOE 60
 QY 61 GNCPEWDGLICWPRGTGCKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
 Db 61 GNCPEWDGLICWPRGTGCKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWA 120
 QY 121 NYSCLRLFLQPDISIGKQFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 Db 121 NYSCLRLFLQPDISIGKQFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYIH 180
 QY 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPONSIEATSVKSYIGCKIAV 240
 Db 181 MHLFVFSFMLRATSIYFKDRVVAHIGVKELESIMODDPONSIEATSVKSYIGCKIAV 240
 QY 241 VMFYFLATNYMILVEGLYLHNLIFVAFPSDTKYLWGFIILGWGFPFAFVAWAVARAT 300
 Db 241 VMFYFLATNYMILVEGLYLHNLIFVAFPSDTKYLWGFIILGWGFPFAFVAWAVARAT 300
 QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
 QY 361 LAKSTLVILVFGVHYIVFVCLPHSFGLGWEIRMHCELFNSFGQFFVSIICYCNGEV 420
 Db 361 LAKSTLVILVFGVHYIVFVCLPHSFGLGWEIRMHCELFNSFGQFFVSIICYCNGEV 420
 QY 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVLTTHSTSSQSVAAAHAWCL---SLAK 477
 Db 421 QAEVKKWSRWNLSDWKRTPPCGSRRCGSLVLTTHSTSSQSVAAAHAWCL---SLAK 477
 QY 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
 Db 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKSPRME 534
 QY 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 9

US-10-295-027-851
 ; Sequence 851, Application US/10295027
 ; GENERAL INFORMATION:
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsberg, Wendy M.
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Glynn, Richard
 ; APPLICANT: Hevezi, Peter A.
 ; APPLICANT: Mack, David H.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Watson, Susan R.
 ; APPLICANT: Eos Biotechnology, Inc.
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

```

; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-851

Query Match          90.6%; Score 2635; DB 28; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

Qy 1 MAMLGASLHWGMLGSCLLARAQLDSGTTTIEEQIVLVKAKVOCELNITAOQGE 60
Db 1 MAMLGASLHWGMLGSCLLARAQLDSGTTTIEEQIVLVKAKVOCELNITAOQGE 60
Qy 61 GNCFFPDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Qy 121 NYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
Db 121 NYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
Qy 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSTEATSVKSYIGCKIAV 240
Db 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSTEATSVKSYIGCKIAV 240
Qy 241 VMFIYFLATNYWILVEGLYLNLIIFVAFSDTKYLMGFFILGNGFPAAFVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYLNLIIFVAFSDTKYLMGFFILGNGFPAAFVAWAVARAT 300
Qy 301 LADARCWELSGADIKWTIQAPILAAIGLNFILFINTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWTIQAPILAAIGLNFILFINTVRVLATKIWETNAVGHDTKQYRK 360
Qy 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVSIYCYNGEV 420
Db 361 LAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSGFQGFVSIYCYNGEV 420
Qy 421 QAEVKGMWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAACWCL---SLAK 477
Db 421 QAEVKGMWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAACWCL---SLAK 480
Qy 478 LPRSPADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
Db 481 IASRQPDSD-----HTLPGVVWSNEQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 534
```

```

Qy 535 SNPDTEG 541
Db 535 SNPDTEG 541

RESULT 10
US-10-404-618-86
; Sequence 86, Application US/10404618
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare M.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Lora, Jose M.
; APPLICANT: White, David
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Robison, Keith E.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL 15571, 2465, 14266, 2882, 52871,
; TITLE OF INVENTION: 8203 AND 16852 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0530MINI
; CURRENT APPLICATION NUMBER: US/10/404,618
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/631,603
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 09/794,763
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,942
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/634,392
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 09/176,075
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/013,634
; PRIOR FILING DATE: 1998-01-26
; PRIOR APPLICATION NUMBER: 09/884,430
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/269,758
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-618-86

Query Match          90.6%; Score 2635; DB 30; Length 550;
Best Local Similarity 91.4%; Pred. No. 5.7e-245;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

Qy 1 MAMLGASLHWGMLGSCLLARAQLDSGTTTIEEQIVLVKAKVOCELNITAOQGE 60
Db 1 MAMLGASLHWGMLGSCLLARAQLDSGTTTIEEQIVLVKAKVOCELNITAOQGE 60
Qy 61 GNCFFPDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTTWA 120
Qy 121 NYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
Db 121 NYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNH 180
Qy 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSTEATSVKSYIGCKIAV 240
Db 181 MHLFVSFMLRATSIYFKDRVVAHIGVKELESIMODDPQNSTEATSVKSYIGCKIAV 240
```

Qy 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARAT 300
 Db 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARAT 300
 Qy 301 LADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYRK 360
 Db 301 LADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYRK 360
 Qy 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGEV 420
 Db 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGEV 420
 Qy 421 QAEVKQWRSRWNLSDVWKRTPPCGSRRCGSLT TTVTHSTSSQSVAAAHAMCL---SLAK 477
 Db 421 QAEVKQWRSRWNLSDVWKRTPPCGSRRCGSLT TTVTHSTSSQSVAAAHAMCL---SLAK 477
 Qy 478 LPRSPADSLTATSLYLAMSQVTCSTASHTLS---TRSNKEDSGRORDIIMKPSRPME 534
 Db 478 LPRSPADSLTATSLYLAMSQVTCSTASHTLS---TRSNKEDSGRORDIIMKPSRPME 534
 Qy 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 11

US-09-826-509-565
 ; Sequence 565, Application US/09826509
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
 ; TITLE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 565
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-565

Query Match 90.4%; Score 2629; DB 23; Length 550;
 Best Local Similarity 91.2%; Pred. No. 2.2e-244;
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;
 Qy 1 MAWLGASLHVWGMWMLGSCLLARAQLDS DGTITIEBOIVLVKAKVQCELNITAOQGE 60
 Db 1 MAWLGASLHVWGMWMLGSCLLARAQLDS DGTITIEBOIVLVKAKVQCELNITAOQGE 60
 Qy 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYD FNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 Db 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYD FNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 Qy 121 NYSCLRFLOPDISIGKQEFCELYMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 Db 121 NYSCLRFLOPDISIGKQEFCELYMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 Qy 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKQSVIGCKIAV 240
 Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKQSVIGCKIAV 240
 Qy 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARAT 300
 Db 241 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARAT 300

Qy 301 LADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYRK 360
 Db 301 LADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYRK 360
 Qy 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGEV 420
 Db 361 LAKSTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGEV 420
 Qy 421 QAEVKQWRSRWNLSDVWKRTPPCGSRRCGSLT TTVTHSTSSQSVAAAHAMCL---SLAK 477
 Db 421 QAEVKQWRSRWNLSDVWKRTPPCGSRRCGSLT TTVTHSTSSQSVAAAHAMCL---SLAK 477
 Qy 478 LPRSPADSLTATSLYLAMSQVTCSTASHTLS---TRSNKEDSGRORDIIMKPSRPME 534
 Db 478 LPRSPADSLTATSLYLAMSQVTCSTASHTLS---TRSNKEDSGRORDIIMKPSRPME 534
 Qy 535 SNPDTEG 541
 Db 535 SNPDTEG 541

RESULT 12

US-10-014-162-110
 ; Sequence 110, Application US/10014162
 ; GENERAL INFORMATION:
 ; APPLICANT: Usdin, Ted B.
 ; APPLICANT: Hoare, Samuel R.J.
 ; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR LIGANDS
 ; FILE REFERENCE: NIH175.001C1
 ; CURRENT APPLICATION NUMBER: US/10/014,162
 ; CURRENT FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/1677
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/139335
 ; PRIOR FILING DATE: 1999-06-15
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 110
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-014-162-110

Query Match 89.4%; Score 2600; DB 26; Length 550;
 Best Local Similarity 90.9%; Pred. No. 1.4e-241;
 Matches 498; Conservative 6; Mismatches 30; Indels 14; Gaps 5;
 Qy 1 MAWLGASLHVWGMWMLGSCLLARAQLDS DGTITIEBOIVLVKAKVQCELNITAOQGE 60
 Db 1 MAWLGASLHVWGMWMLGSCLLARAQLDS DGTITIEBOIVLVKAKVQCELNITAOQGE 60
 Qy 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYD FNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 Db 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYD FNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
 Qy 121 NYSCLRFLOPDISIGKQEFCELYMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 Db 121 NYSCLRFLOPDISIGKQEFCELYMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
 Qy 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKQSVIGCKIA 239
 Db 181 MHLFVSFMLRATSI FVKDRVVAHIGVKELESIMODDPQNSIEATSVKQSVIGCKIA 240
 Qy 240 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARA 299
 Db 240 VMFIYFLATNYWILVEGLYHLNLI FVAFFSDTKYLMGFFILIGWGPFAAFVAAWAVARA 299
 Qy 300 TLADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYR 359
 Db 300 TLADARCWELSGADIKWYQAPILAAI GLNFIPLNTVRVLA TKIWNETHAVGHDTRKQYR 359
 Qy 360 KLAESTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGE 419
 Db 360 KLAESTLVILVFGVHYIVFVCLPHSFTGLGWEIRMECELFFNSFOGFFVSIYCYCNGE 419

Db 360 KLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYYCYCNCE 419
QY 420 VQAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLA 476
Db 420 VQAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLA 479
QY 477 KLPRSPADSLTATSLYLAWSGVQTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 533
Db 480 KIASRQPDG-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 533
QY 534 ESNPDTEG 541
Db 534 ESNPDTEG 541

RESULT 13

US-60-245-228-218
; Sequence 218, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 218
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HUMAN
US-60-245-228-218

Query Match 89.0%; Score 2586; DB 32; Length 593;
Best Local Similarity 90.5%; Pred. No. 3.5e-240;
Matches 495; Conservative 6; Mismatches 30; Indels 16; Gaps 5;

QY 1 MAMLGASLHVWGLMLGSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITQAQOGE 60
Db 48 MAGLGASLHVWGLMLGSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITQAQOGE 107
QY 61 GNCPEWDGLICWPRTGVGKISAVPCPPYIYDFNHKGVAFRHCPNPGTWFDMHSLNKTWA 120
Db 108 GNCPEWDGLICWPRTGVGKISAVPCPPYIYDFNHKGVAFRHCPNPGTWFDMHSLNKTWA 167
QY 121 NYSCLRFLOPDISIGKQEFPERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 180
Db 168 NYSCLRFLOPDISIGKQEFPERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 227
QY 181 MHLFVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSGYIGCKIAV 240
Db 228 MHLFVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSGYIGCKIAV 287
QY 241 VMFIYFLATNYWTLVVEGLYLHNLIFVAFPSDTKYLWGFFILIGWFFPAAFFVAAWAVARAT 300
Db 288 VMFIYFLATNYWTLVVEGLYLHNLIFVAFPSDTKYLWGFFILIGWFFPAAFFVAAWAVARAT 345
QY 301 LADARCWELSGADIKWYIQAIPILAAIIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
Db 346 LADARCWELSGADIKWYIQAIPILAAIIGLNFILNTVRLATKIWETNAVGHDTKQYRK 403
QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYYCYCNCE 420
Db 404 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYYCYCNCE 463
QY 421 QAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 477
Db 464 QAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 523
QY 478 LPRSPADSLTATSLYLAWSGVQTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
Db 524 IASRQPDG-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 577

RESULT 15

US-10-126-052A-661
; Sequence 661, Application US/10126052A

QY 535 SNPDTEG 541
Db 578 SNPDTEG 584

RESULT 14

US-60-258-272-90
; Sequence 90, Application US/60258272
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL0001041
; CURRENT APPLICATION NUMBER: US/60/258,272
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HUMAN
US-60-258-272-90

Query Match 89.0%; Score 2586; DB 32; Length 593;
Best Local Similarity 90.5%; Pred. No. 3.5e-240;
Matches 495; Conservative 6; Mismatches 30; Indels 16; Gaps 5;

QY 1 MAMLGASLHVWGLMLGSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITQAQOGE 60
Db 48 MAGLGASLHVWGLMLGSCLLARAQLDSDGTITIEEQIVLVKAKVQCELNITQAQOGE 107
QY 61 GNCPEWDGLICWPRTGVGKISAVPCPPYIYDFNHKGVAFRHCPNPGTWFDMHSLNKTWA 120
Db 108 GNCPEWDGLICWPRTGVGKISAVPCPPYIYDFNHKGVAFRHCPNPGTWFDMHSLNKTWA 167
QY 121 NYSCLRFLOPDISIGKQEFPERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 180
Db 168 NYSCLRFLOPDISIGKQEFPERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIH 227
QY 181 MHLFVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSGYIGCKIAV 240
Db 228 MHLFVSFMLRATSFVKDRVVHAHIGVKELESIMQDDPONSIEATSVKSGYIGCKIAV 287
QY 241 VMFIYFLATNYWTLVVEGLYLHNLIFVAFPSDTKYLWGFFILIGWFFPAAFFVAAWAVARAT 300
Db 288 VMFIYFLATNYWTLVVEGLYLHNLIFVAFPSDTKYLWGFFILIGWFFPAAFFVAAWAVARAT 345
QY 301 LADARCWELSGADIKWYIQAIPILAAIIGLNFILNTVRLATKIWETNAVGHDTKQYRK 360
Db 346 LADARCWELSGADIKWYIQAIPILAAIIGLNFILNTVRLATKIWETNAVGHDTKQYRK 403
QY 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYYCYCNCE 420
Db 404 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRHCELFNFNSFQGFVSIYYCYCNCE 463
QY 421 QAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 477
Db 464 QAEVKKQWRNLSVDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL----SLAK 523
QY 478 LPRSPADSLTATSLYLAWSGVQTSRTASHTLS---TRSNKEDSGRQDDILMEKPSRPM 534
Db 524 IASRQPDG-----HITLPGVWNSQDCLPHSFHEETKEDSGRQDDILMEKPSRPM 577
QY 535 SNPDTEG 541
Db 578 SNPDTEG 584


```
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Murray, Richard
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and
; FILE REFERENCE: 018501-001530US
; CURRENT APPLICATION NUMBER: US/10/126,052A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/284,770
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/290,492
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/339,245
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,370
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 691
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 661
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-126-052A-661

Query Match      86.4%; Score 2513; DB 27; Length 561;
Best Local Similarity 91.2%; Pred. No. 3.7e-233;
Matches 477; Conservative 6; Mismatches 28; Indels 12; Gaps 3;

QY 25 QLDSDGTTTIEEQIVLVKAKVOCBLNITAOLEGNGCPPEWDGLICWPRGTGKISAV 84
Db 36 QLDSDGTTTIEEQIVLVKAKVOCBLNITAOLEGNGCPPEWDGLICWPRGTGKISAV 95

QY 85 PCPPYIYDFNHKGVAFPHCNPGTWDPMHSLNKTWANYSDCLRFLOPDISIGKQEFCE 144
Db 96 PCPPYIYDFNHKGVAFPHCNPGTWDPMHSLNKTWANYSDCLRFLOPDISIGKQEFCE 155

QY 145 YVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHMLFVSFMLRATSI FVKDRVVH 204
Db 156 YVMYTVGYSISFGSLAVAILIIGYFRRLHCTRYNHMLFVSFMLRATSI FVKDRVVH 215

QY 205 IGVKELESIMQDDPQNSIATSVDSQYIGCKIAVVMFIYFLATNYWILVEGLYHNL 264
Db 216 IGVKELESIMQDDPQNSIATSVDSQYIGCKIAVVMFIYFLATNYWILVEGLYHNL 275

QY 265 IFVAFPSDTKYLWGFLLIGWGPFAAFVAWAVARATLADARCWELSGADIKWIYQAPILA 324
Db 276 IFVAFPSDTKYLWGFLLIGWGPFAAFVAWAVARATLADARCWELSGADIKWIYQAPILA 335

QY 325 AIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVFGVHYIVFVCLPH 384
Db 336 AIGLNFILFNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVFGVHYIVFVCLPH 395

QY 385 SFTGLGWEIRMECELPFNFGQFFVSIYCYNGEVQAEVKRWGRNLSVDWKRTPPCG 444
Db 396 SFTGLGWEIRMECELPFNFGQFFVSIYCYNGEVQAEVKRWGRNLSVDWKRTPPCG 455

QY 445 SRRCGSVLTVTHSTSSQVAAAHAWCL--SLAKLPRSPADSLTATSLYLAMSGVTOS 501
Db 456 SRRCGSVLTVTHSTSSQVAAAHAWCL--SLAKLPRSPADSLTATSLYLAMSGVTOS 509

QY 502 RTASHTLS---TRSNKDSGRDDILMEKSPRPMESNPDTEG 541
Db 510 NSEQDCLPHSFHEETKEDSGRQDDILMEKSPRPMESNPDTEG 552
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:23:14 ; Search time 17 Seconds

(without alignments)
1496.556 Million cell updates/sec

Title: US-09-996-569-2

Perfect score: 2907

Sequence: 1 MAWLGA SLHWGMLGSL.....DDLMEKPSRPMESNPDTEG 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2635	90.6	550	1 PTR2 HUMAN	P49190 homo sapien
2	2213.5	76.1	546	1 PTHR RAT	P70555 rattus norv
3	1397	48.1	585	1 PTHR_DIDMA	P25107 didephis m
4	1345	46.3	585	1 PTHR_PIG	P50133 sus scrofa
5	1336.5	46.0	593	1 PTHR HUMAN	Q03431 homo sapien
6	1331.5	45.8	591	1 PTHR RAT	P25961 rattus norv
7	1324	45.5	591	1 PTHR MOUSE	P41593 mus musculus
8	801	27.6	449	1 SCRC RAT	P23811 rattus norv
9	794	27.3	445	1 SCRC RABIT	O46502 oryctolagus
10	793	27.3	457	1 VIPR_MELGA	Q91085 meleagris g
11	791.5	27.2	459	1 VIPR_MOUSE	P97751 mus musculus
12	785	27.0	458	1 VIPR_PIG	Q28992 sus scrofa
13	784	27.0	440	1 SCRC HUMAN	P47872 homo sapio
14	782	26.9	447	1 VIPR CARAU	Q90308 carassius a
15	772.5	26.6	459	1 VIPR RAT	P30083 rattus norv
16	759.5	26.1	457	1 VIPR HUMAN	P32241 homo sapien
17	713.5	24.5	437	1 VIPR_MOUSE	P41588 mus musculus
18	708	24.4	437	1 VIPR RAT	P35000 rattus norv
19	702	24.1	438	1 VIPR HUMAN	P41587 homo sapien
20	685	23.6	468	1 PACR_HUMAN	P41586 homo sapien
21	677.5	23.3	496	1 PACR_MOUSE	P70205 mus musculus
22	673.5	23.2	513	1 PACR_BOVIN	Q29627 bos taurus
23	667.5	23.0	523	1 PACR RAT	P32215 rattus norv
24	665	22.9	550	1 GLP2 RAT	Q920W0 rattus norv
25	663	22.8	489	1 GLP1_MOUSE	O35659 mus musculus
26	662	22.8	462	1 GIPR_MESAU	P43218 mesocricetu
27	655	22.5	463	1 GLP1_RAT	P32301 rattus norv
28	641.5	22.1	466	1 GIPR_HUMAN	P48546 homo sapien
29	635.5	21.9	553	1 GLP2_HUMAN	Q95838 homo sapien
30	630.5	21.7	423	1 GRFR_HUMAN	O02643 homo sapien
31	628.5	21.6	463	1 GLP1_HUMAN	P43220 homo sapien
32	622.5	21.4	423	1 GRFR_PIG	P34999 sus scrofa
33	619	21.3	477	1 GLR_HUMAN	P47871 homo sapien

34	616	21.2	455	1 GIPR RAT	P43219 rattus norv
35	607	20.9	485	1 GLR RAT	P30082 rattus norv
36	596.5	20.5	423	1 GRFR MOUSE	P32082 mus musculus
37	595	20.5	485	1 GLR MOUSE	O61606 mus musculus
38	594.5	20.5	478	1 CALR_CAVPO	O08893 cavia porce
39	589.5	20.3	515	1 CALR_MOUSE	Q60755 mus musculus
40	581	20.0	516	1 CALR RAT	P32214 rattus norv
41	579.5	19.9	490	1 CALR HUMAN	P30988 homo sapien
42	576	19.8	474	1 CALR RABIT	P79222 oryctolagus
43	574	19.7	464	1 GRFR RAT	Q02644 rattus norv
44	554.5	19.1	420	1 CRFL_CHICK	Q90812 gallus gall
45	544.5	18.7	498	1 CALR_PIG	P25117 sus scrofa

ALIGNMENTS

RESULT 1
PTR2_HUMAN
ID PTR2_HUMAN STANDARD; PRT; 550 AA.
AC P49190;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parathyroid hormone receptor precursor (PTH2 receptor).
GN PTHR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=95318121; PubMed=7797535;
RA Usdin T.B., Gruber C., Bonner T.I.;
RT Identification and functional expression of a receptor selectively
RT recognizing parathyroid hormone, the PTH2 receptor.";
RL J. Biol. Chem. 270:15455-15458 (1995).
RN [2]
RP SEQUENCE OF 26-40 AND 306-550 FROM N.A.
RX MEDLINE=97079671; PubMed=8921382;
RA Usdin T.B., Modi W., Bonner T.I.;
RT "Assignment of the human PTH2 receptor gene (PTHR2) to chromosome 2q33
RT by fluorescence in situ hybridization.";
RL Genomics 37:140-141 (1996).
CC -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE.
CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.
CC -!- ALSO EXPRESSED IN THE TESTIS.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U25128; AAC50157.1; -;
CC EMBL; U47124; AAA96796.1; -;
CC EMBL; U47129; AAC50767.1; -;
CC EMBL; U47125; AAC50767.1; JOINED.
CC EMBL; U47126; AAC50767.1; JOINED.
CC EMBL; U47127; AAC50767.1; JOINED.
CC EMBL; U47128; AAC50767.1; JOINED.
CC PIR; A57519; A57519.
CC Genew; HGNC:9609; PTHR2.
CC MIM; 601469; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.


```

FT TRANSMEM 392 414 7 (POTENTIAL)
FT DOMAIN 415 546 CYTOPLASMIC (POTENTIAL)
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

Query Match 76.1%; Score 2213.5; DB 1; Length 546;
Best Local Similarity 76.5%; Pred. No. 8.5e-162;
Matches 416; Conservative 37; Mismatches 82; Indels 9; Gaps 4;

QY 1 MAWLGLSHVGMWMLGSCLLARQAQLDSGTITIEEQIVLVKAKVQCELNITTAQLQEGE 60
Db 1 MPWLEALPYICGWLIIILRSCLLVCAQLDSGTITIEEQIVLVKAKVQCELNITTAQLQEGE 60

QY 61 GNCFFPDWGLICWPRGTGVKISAVPCPPYIYFNHKGVAFRHCPNPNGTWDFMHSLNKTWA 120
Db 61 GNCFFPDWGLICWPRGTAGTSAMPCCSYVDNFHKGVAFRHCTPNGTWDFHGSNKTWA 120

QY 121 NYSDCLRFLOPDISIGKQFCERLYVMYTVGHSISFGSLAVAILIIGYFRRLHCTRNYIH 180
Db 121 NYSDC--FLQPDINIGKQFFENLYITVGVHSISFGSLAVAILIIGYFRRLHCTRNYIH 178

QY 181 MHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMODDPONSIATSVDSKVIGCKIAV 240
Db 179 LHLFVSFMLRATSIKVDKRVVHAHIGVKELESIMODDPONSIATSVDSKVIGCKIAV 238

QY 241 VMFIYFATNYWILVEGLYLHNLIFVAFPSFTKYLWGFILGWGFPAAFAVAWAVARAT 300
Db 239 VMFIYFATNYWILVEGLYLHNLIFVSFFSTKYLWGFILGWGFPAAFAVAWAVARAT 298

QY 301 LADARCWELSGDIKWIYQAPILAAIGLAFILFNTVRVLATKIWETNAVGHDTKQYRK 360
Db 299 LADTRCWELSGAD--RWIYXXPILAAIGLAFILFNTVRVLATKIWETNAVGHDMRKQYRK 357

QY 361 LAKSTLVLVVFGVHVIVFVCLPHSFTGLWEIRHCELFENSFQGFVSVIICYCNGEV 420
Db 358 LAKSTLVLVVFGVHVIVFVCLPHSFTGLWEIRHCELFENSFQGFVSVIICYCNGEV 417

QY 421 QAEVKMWRNLSVDWVKRTPPCGSRRCGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 480
Db 418 QAEVKMTWRNLSIDWKAPPGCGHRYGSLVTTVTHSTSSQVAAAHAWCLSLAKLPR 477

QY 481 SPA---DSLTAISLYLAMSGVTSRTASHTLSRNSKSGRQDDILMEKPSRPMESNP 537
Db 478 TACRQIDSHVTLPGYVWSSEQDCQPQS---TPEETKKGHGRQDDSPVGESSRPVAFIT 534

QY 538 DTEG 541
Db 535 DTEG 538

```

RESULT 3

```

PTHR_DIDMA
ID PTHR_DIDMA STANDARD; PRT; 585 AA.
AC P25107;
DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor).
GN PTHRI OR PTHR.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92054592; PubMed=1658941;
RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;

```

```

RT "A G protein-linked receptor for parathyroid hormone and parathyroid
RL hormone-related peptide";
Science 254:1024-1026(1991).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch)
CC
CC EMBL; M74445; AAA30979.1; -.
DR FIR; A39286; A39286.
DR HSP; Q03431; 1EL1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 585
FT PARATHYROID HORMONE/PARATHYROID HORMONE-
FT RELATED PEPTIDE RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT 1 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 2 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 3 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 4 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 5 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT 6 (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT 7 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 585 AA; 65963 MW; 34900384CD6DF477 CRC64;

Query Match 48.1%; Score 1397; DB 1; Length 585;
Best Local Similarity 48.0%; Pred. No. 2.3e-99;
Matches 275; Conservative 94; Mismatches 134; Indels 70; Gaps 10;

QY 24 AQLSDGVTITIEEQIVLVKAKVQCELNIT--
Db 24 ALVDADDVITKEEQIILLRNAQCEQLKVELRVPELAESAQDWMSRSAKTKKPKAEK 83

QY 54 --AQLQEG-----EGNCFPEWDLICWPRTGVGKISAVPCPPYIYFNHKGVAFR 101
Db 84 LYSQAEESESVDSRSLQDGLFPEWDLICWPRTGVGKISAVPCPPYIYFNHKGVAFR 143

QY 102 HCNPNGTWDFMHSLNKTWANYSDCLRFLOPDISIGKQFCERLYVMYTVGHSISFGSLAV 161

```

```

Db 144 RCDNSGSELVGNRRNTWANYSECVKLTNETR--EREVDFRLGMVTVGVSYSLGSLTV 201
Qy 162 AILIGYFRRLLHCTRNTHMLFVSFMLRATSIKDKRVVHAHIGVKELESIMODPON 221
Db 202 AVILIGYFRRLLHCTRNTHMLFVSFMLRAVSIKDAVLSGVSTDEIER-ITEBELRA 260
Qy 222 SIEATSDVKSGYICCKIAVNFIVFLATNYYWILVEGLYHLNLFVAFPSDTKYLWGFIL 281
Db 261 FTEPPADKAGFVGCRAVTVFLVLTNYYWILVEGLYHLNLFVAFPSDTKYLWGFIL 320
Qy 282 IGMFPAFAVAWAATLADACWELSGADIIWYQAPILAAIGLNFILNLTNRVLA 341
Db 321 FGMGLPAFAVAVVTVATLANTECWLSSGNKKWIIQVPLAAVNVNFIINIRVLA 380
Qy 342 TKIMETNAVGHDTKQYRKLAISTLVLVVFGVHIVFVCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKLRETNAAGCDTRQYRKLLKSLVLMPLFEGVHYIVFMATPYTEVSGIILVQVGMVEM 440
Qy 401 FNSFGQFVSIYCYCNGEVOAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTH--- 457
Db 441 FNSFGQFVSIYCYCNGEVOAEVKWMSRWNLSDVMKRTPPCGSRRCGSLVTTVTH--- 493
Qy 458 -STSSQVQAAAHAWCLSLAKLPRSPADSLTATSLYMSGVTSQRTASHTLSTRNKED 516
Db 494 VSHTSVTNVPGRGLALSLS--PRLAPGAGASANGHQLFGYVKHGSISEN-SLPSSGPE 550
Qy 517 SGRORDILM-----EKSPRPMESNPD 539
Db 551 PGKDDGLNGSLYEPVNGEQPPLLEERET 583

RESULT 4
PTRR_PIG
ID PTRR_PIG STANDARD; PRT; 585 AA.
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor).
GN PTHr1 OR PTHr.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor."
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10315; AAC48619.1; -.
CC HSSP; Q03431; IBL1.

```

```

DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 27 585
FT PT
FT DOMAIN 27 184
FT TRANSMEM 185 208
FT DOMAIN 209 215
FT TRANSMEM 216 235
FT DOMAIN 236 277
FT TRANSMEM 278 301
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT DOMAIN 424 435
FT TRANSMEM 436 458
FT DOMAIN 459 585
FT DISULFID 48 113
FT DISULFID 104 144
FT DISULFID 127 166
FT CARBOHYD 147 147
FT CARBOHYD 157 157
FT CARBOHYD 162 162
FT CARBOHYD 172 172
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 46.3%; Score 1345; DB 1; Length 585;
Best Local Similarity 52.5%; Pred. No. 2.2e-95;
Matches 259; Conservative 75; Mismatches 101; Indels 58; Gaps 7;

Qy 4 LGASLHVWGMILGSCLL---ARAQLSDSGTITIEBQIVLVKAKVQCELNITAQLQ--- 57
Db 1 MGAARIAPGLALLCCPVLLSAYALVADDVMTKESQIFLLHRAQAQCEKELAVLORPA 60
Qy 58 -----ELEGN-----CPENDGLICWPGTVG 79
Db 61 DIMESDKGNASAPTSKPKREKASGLYPESGSDTSGRHQGRFCPLPEWDHILCWPLGAPG 120
Qy 80 KISAVPCPPYIYDFNHKGVAFRHCPNPGTWDFMHSNKTWANYSDCLRFLOPDISIGKOE 139
Db 121 EVVAMPCPYIYDFNHKGHAYRCDNGSWELVPGHNRWTWANYSECVKLTNETR--ERE 178
Qy 140 FCERLYMYTVGVSYISFGSLAVAILIIGYFRRLHCTRNTHMLFVSFMLRATSIKVKOR 199
Db 179 VFDRLGMIYTVGVSYSLASLTAVLILAYFRRLHCTRNTHMLFVSFMLRAVSIKVKDA 238
Qy 200 VVHAHIGVKELESIMQD-----DPQNSIEATSDVKSGYICGKIADVMIPIFLATNYYW 253
Db 239 VLYSGATLDEAERLTTEEELRAIAQAFLPFFVAATS-----YVGCRAVTVFLYFLATNYYW 293
Qy 254 ILVEGLYHLNLFVAFPSDTKYLWGFILGWGFPAAFAVAWAVARATLADARCEWELSGAD 313
Db 294 ILVEGLYHLNLFVAFPSDTKYLWGFILGWGFPAAFAVAWAVARATLADARCEWELSGAD 353
Qy 314 IKWYQAPILAAIGLNFILNLTNRVLA TKIMETNAVGHDTKQYRKLAISTLVLVVFG 373
Db 354 KKWIIQVPLASIVLNFIINIRVLA TKLRETNAAGCDTRQYRKLLKSLVLMPLFEG 413
Qy 374 VHYIVFVCLPHS-FTGLGWEIRMHCELFNPSFGQFVSIYCYCNGEVOAEVKWMSRW 432
Db 414 VHYIVFVCLPHS-FTGLGWEIRMHCELFNPSFGQFVSIYCYCNGEVOAEVKWMSRW 473

```

QY 433 LSVDWKRTPPCGS 445
Db 474 LALDFKRRSGS 486

RESULT 5
ID PTHR HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor).
GN PTHr OR PTHr.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93238641; PubMed=8386612;
RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Identical complementary deoxyribonucleic acids encode a human renal
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
RL Endocrinology 132:2157-2165(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93387403; PubMed=8397094;
RA Schneider H., Feyen J.-H., Rao Movva N.;
RT "Cloning and functional expression of a human parathyroid hormone
RT receptor.";
RL Eur. J. Pharmacol. 246:149-155(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95263723; PubMed=7745008;
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtko J., Dop C.,
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the
RT coding exons of the human parathyroid hormone (PTH)/PTH-related
RT peptide receptor gene.";
RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Levine M.A.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
RX MEDLINE=20374568; PubMed=10913300;
RA Grauchopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
RA Schafer W., Rucknagel K.P., Rudolph R.;
RT "The N-terminal fragment of human parathyroid hormone receptor 1
RT constitutes a hormone binding domain and reveals a distinct disulfide
RT pattern.";
RL Biochemistry 39:8878-8887(2000).
RN [6]
RP STRUCTURE BY NMR OF 168-198.
RX MEDLINE=98409426; PubMed=9737850;
RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
RT "Binding domain of human parathyroid hormone receptor: from
RT conformation to function.";
RL Biochemistry 37:12737-12743(1998).
RN [7]
RP VARIANT MURK-JANSEN ARG-223.
RX MEDLINE=95215874; PubMed=7701349;
RA Schipani E., Kruse K., Juppner H.

RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
RT metaphyseal chondrodysplasia.";
RL Science 268:98-100(1995).
RN [8]
RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
RX MEDLINE=96366745; PubMed=87031170;
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Juppner H.;
RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";
RL New Engl. J. Med. 335:708-714(1996).
RN [9]
RP MUTAGENESIS OF ARG-223 AND PRO-410.
RX MEDLINE=97322091; PubMed=9178745;
RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
RA Juppner H.;
RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";
RL Mol. Endocrinol. 11:851-858(1997).
RN [10]
RP FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC [11]
RP SUBCELLULAR LOCATION: Integral membrane protein.
CC [12]
RP TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
CC KIDNEY, BONE AND LIVER.
CC [13]
RP DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF BLOWSTRAND TYPE OF
CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
CC [14]
RP DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF MURK-JANSEN TYPE OF
CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
CC HORMONES.
CC [15]
RP SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
RN [16]
EMBL; L04308; AAA36525.1; --
EMBL; X68596; CAA48589.1; --
EMBL; U22409; AAB60657.1; --
EMBL; U22401; AAB60657.1; JOINED.
EMBL; U22402; AAB60657.1; JOINED.
EMBL; U22403; AAB60657.1; JOINED.
EMBL; U22404; AAB60657.1; JOINED.
EMBL; U22405; AAB60657.1; JOINED.
EMBL; U22406; AAB60657.1; JOINED.
EMBL; U22407; AAB60657.1; JOINED.
EMBL; U22408; AAB60657.1; JOINED.
EMBL; U17418; AAA56774.1; --
PIR; I38139; A49191.
PDB; 1BU1; 30-MAR-99.
PDB; 1ET2; 06-SEP-00.
PDB; 1ET3; 06-SEP-00.
Genew; HGNC:9608; PTHR1.
MIM; 168468; --
MIM; 156400; --
MIM; 215045; --
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
GO; GO:0001501; P:skeletal development; TAS.


```

or send an email to license@isb-sib.ch.
-----
CC EMBL; M7184; AAA41811.1; --
CC EMBL; L19475; AAA68098.1; --
CC PIR; I54195; I54195.
CC HSSP; Q03431; 1BL1.
CC InterPro; IPR000832; GPCR secretin.
CC DR InterPro; IPR001879; hormn_receptor.
CC DR Pfam; PF00002; 7tm_2; 1.
CC DR Pfam; PF02793; HEM1_1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR SMART; SM00008; Hormr; 1.
CC DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
CC DR PROSITE; PS00650; G PROTEIN RECP F2_2; 1.
CC DR PROSITE; PS00227; G PROTEIN RECP F2_3; 1.
CC DR PROSITE; PS00261; G PROTEIN RECP F2_4; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; signal.
CC SIGNAL 1 26
CC FT CHAIN 27 591
CC FT PARATHYROID HORMONE/PARATHYROID HORMONE-
CC FT RELATED PEPTIDE RECEPTOR.
CC FT DOMAIN 27 188
CC FT TRANSMEM 189 212
CC FT DOMAIN 213 219
CC FT TRANSMEM 220 239
CC FT DOMAIN 240 282
CC FT TRANSMEM 283 306
CC FT DOMAIN 307 320
CC FT TRANSMEM 321 342
CC FT DOMAIN 343 361
CC FT TRANSMEM 362 382
CC FT DOMAIN 383 409
CC FT TRANSMEM 410 428
CC FT DOMAIN 429 440
CC FT TRANSMEM 441 463
CC FT DOMAIN 464 591
CC FT DISULFID 48 117
CC FT DISULFID 108 148
CC FT DISULFID 131 170
CC FT CARBOHYD 151 151
CC FT CARBOHYD 161 161
CC FT CARBOHYD 166 166
CC FT CARBOHYD 176 176
CC FT SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;
Query Match 45.8%; Score 1331.5; DB 1; Length 591;
Best Local Similarity 46.6%; Pred. No. 2.3e-94;
Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;
QY 22 ARAQLDSGDTTIEBQIVLVKAKVCE-----LNIATQLOEGGN----- 62
Db 22 AYALVDADDVFTKEBQIFLLHRAQAQCDKLLKEVLHTAANIMESDKGWTPASTSGKPKBE 81
QY 63 -----CFPEWDGLICWPRTGVTKISAVPCPPYIYDFNHK 96
Db 82 KASGKFYSPESKENKDVPVTSRRGRPCLPENDNIVCWPLGAGVAVVPCPYIYDFNHK 141
QY 97 GVAFRCNPGNCTWDFMHLNKTWANYSDCLRPDIDISIGKQFCEFLRYVMYTVGYSISF 156
Db 142 GHAYRRCDRNGSWVPGHNRTWANYSECLKENTNETR--EREVDRLGMIVTVGYSMSL 199
QY 157 GSLAVAILLIGYFRILHCTRNVIHMLFVSFMLRATSIKVDQVVAHIGVKELESLESL--- 213
Db 200 ASLTAVALLAYFRRLHCTRNVIHMLFVSFMLRATSIKVDQVVAHIGVKELESLESL--- 259
QY 214 -----IMQDDPQNSIEATSVKSGYIGCKIAVMVFYFLATNYIWLVEGLYHLNLI FVAF 269
Db 260 ELHITAQVPPPPAAAANG-----YAGCRVAVTFYFLATNYIWLVEGLYHLNLI FVAF 314
QY 270 FSDTKYINGFILIIGNGFFPAFVAWAVARATLADARWELSGADIKWIYQAFILAAIGLN 329
Db 315 FSEKYLGLGFTIFGNGLPAFVAVVWVGRATLANTGCDLSSGKHKKI IQVPIIASVLN 374
QY 330 FILFLNTVRVLATKTIWEINAVGHDTRKQYRKLAKSTLVLVLFVGVHYIVFVCLPHS-FTG 388
-----
Db 375 FILFINIIRVLATKRIETNAGRCDDTQQYRKLRSLVLVPLFGVHYTFMALPYTEVSG 434
QY 389 LGWEIRMCLEFNSFGQFFVSIYCYCNGEVQVQVAKWMSRWNLSDVMKRTTPPCGSRRC 448
Db 435 TLWQIQMHWEMLFNSFGQFFVSIYCYCNGEVQVQVAKWMSRWNLSDVMKRTTPPCGSRRC 494
QY 449 GSVLTVTHSTSSQSVAAHAWCLSLAKLPRSPADSLTATSLYLSMSG-----VTQS 501
Db 495 -SYGPMVSHTSVTNVGFRAG---LSLPLSPRLPP---ATTNGHSQLPGHAKPGAPATET 546
QY 502 RTASHTLSTRS-----NKEDSGRQRDDIIMEX 528
Db 547 ETLPVTMAVPKDDGLNGSCGLDEASGSARPPPLQEQ 585
-----
RESULT 7
PTRR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHr receptor).
GN PTHRI OR PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEHA;
RC MEDLINE=95034305; PubMed=7524627;
RA Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone
RT related peptide receptor mRNA in mouse postimplantation embryos
RT indicates involvement in multiple developmental processes.";
RL Mech. Dev. 47:29-42(1994).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALEB/C;
RC MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC CC FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC CC SUBCELLULAR LOCATION: Integral membrane protein.
CC CC SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC EMBL; X78936; CAAS536.1; --
CC EMBL; L34611; AAA40011.1; --
CC EMBL; L34608; AAA40011.1; JOINED.
CC EMBL; L34607; AAA40011.1; JOINED.
CC EMBL; L34609; AAA40011.1; JOINED.
CC EMBL; L34610; AAA40011.1; JOINED.
CC PIR; I59297; I59297.
CC PIR; S44203; S44203.
CC HSSP; Q03431; 1BL1.

```


[illegible]

FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;

Query Match 27.6%; Score 801; DB 1; Length 449;
Best Local Similarity 37.3%; Pred. No. 6e-54;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 14 LMLGSCCLARAQLSDSGTITIEBQIVLVKAKVQCELNITAQL-QBEGNCPE----- 66
Db LLLRLLLTKAA-----HTGVPRPLCDVRVLBERAHCLQLSKKKGALGPETASGCE 67

QY 67 --WDGLICWPRGTGKISAVCPPIYDFNHK-GVAFRHCNPNGTWDFMHSLNKTNWYNS 123
Db GLWDMNSCWPSAPARTVEVQCPKFLMLSNKNGSLFRNCTQDG-----WSB-- 114

QY 124 DCLRFLOPDISG---KQFCER-----LYVMVTGYSISFGSLAVAILIGVFRRLH 173
Db ---TFPRDLACGVNINNSFNERRHAYLLKLMVTVGYSSSLMALLVALSLCSFRRLLH 171

QY 174 CTRNYIHMLFVSFMLRATSIIVKORVVAHIGVKELESIMQDDPQNSIEATSDKSOY 233
Db CTRNYIHMLFVSFILRALSNIKAV-----LFSDD-----VTYCD-AHK 212

QY 234 IOCKIAVMTFVFLATNYWILVEGLYLNLIIVAFPSDTKYLWGLFGFPAFVA 293
Db VGCKLVMTFVFCIMANYAWLLVEGLYLNLIIVAFPSDTKYLWGLFGFPAFVA 272

QY 294 WAVARATLADARCWELSA-GDIKWTYQAPILAAIGLNFILNTVRLATKIWETNAUGH 352
Db WAITHFLENTGCWDINANASVWVIRGEVILSILNFIFFINILRILMKLRTQSTRGS 332

QY 353 DTRKYRKLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFGFVSI 412
Db ET-NHYKRLAKSTLLIPLFGHYIVAFSPED-----AMEVOLFELALGSGFGLVAVL 387

QY 413 YCYCNGEVOAEYKKNWSNLSVDWKRTPPCGSRRCGSLVTVTHSTSSQS 464
Db YCFLNGEVOLEQKKWRQWHLQ-EPLPRVAENNSFNATNGPHTSTKASTE 438

RESULT 9
SCRC_RABIT
ID SCRC_RABIT STANDARD; PRT; 445 AA.
AC O46502;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Secretin receptor precursor (SCT-R).
GN SCRT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxID=9986;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98366112; PubMed=9700755;
RA Svoboda M., Tastenoj M., de Neef P., Delpoer C., Waelbroeck M.,
RA Robberecht P.;
RT "Molecular cloning and in vitro properties of the recombinant rabbit
RT secretin receptor."
RL Peptides 19:1055-1062 (1998).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF025411; AAC32767.1; --
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm.2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G-PROTEIN RECEP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN RECEP_F2_2; 1.
DR PROSITE; PS00227; G-PROTEIN RECEP_F2_3; 1.
DR PROSITE; PS00261; G-PROTEIN RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 445
FT DOMAIN 22 139
FT TRANSMEM 140 163
FT DOMAIN 164 170
FT TRANSMEM 171 190
FT DOMAIN 191 212
FT TRANSMEM 213 236
FT DOMAIN 237 250
FT TRANSMEM 251 272
FT DOMAIN 273 290
FT TRANSMEM 291 313
FT DOMAIN 314 339
FT TRANSMEM 340 358
FT DOMAIN 359 365
FT TRANSMEM 366 388
FT DOMAIN 389 445
FT CARBOHYD 68 68
FT CARBOHYD 96 96
FT CARBOHYD 102 102
FT CARBOHYD 124 124
SQ SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;

Query Match 27.3%; Score 794; DB 1; Length 445;
Best Local Similarity 37.4%; Pred. No. 2e-53;
Matches 182; Conservative 71; Mismatches 135; Indels 98; Gaps 17;

QY 13 WMLGSCCLARAQLSDSGTITIEBQIVLVKAKVQCELNITAQLQEGNGCPPE----- 66
Db WLLIGFACAAH-----LVGAPRLCD--VLWVLOEERDQCLQELERERL 53

QY 67 -----WDGLICWPRGTGKISAVCPPIYDF-NHKGVAFRHCNPNGTWDFMH 113
Db GEEQVPVCGQGLWDMNSCWPSAPGRVVELECPFLMLTNSGSLFRNCTQDG----- 107

QY 114 SLNKTWANSCLRFLOPDISG-----KQFCERLYVMVTGYSISFGSLAVAI 163
Db -----WTE-----TFPRDLACGVNINNSFNERRHAYLLKLMVTVGYSSSLMALLVAL 157

QY 164 LIIGYFRRLHCTRYNIHMLFVSFMLRATSIIVKORVVAHIGVKELESIMQDDPQNSI 223
Db GILCAFRRLHCTRYNIHMLFVSFMLRATSIIVKORVVAHIGVKELESIMQDDPQNSI 200

QY 224 EATSVDSKSOYIGCKIAVMTFVFLATNYWILVEGLYLNLIIVAFPSDTKYLWGLFG 283
Db -----AHCID-AHRVGCKLVMTFVFCIMANYAWLLVEGLYLNLIIVAFPSDTKYLWGLFG 258

QY 284 WGFPAFVAWAVARATLADARCWELSA-GDIKWTYQAPILAAIGLNFILNTVRLAT 342
Db WGSFAMFVTSWAVTRHFLSDSGCWDINANAAIWWVIRGPVILSILNFIINILRILTR 318

QY 343 KINETNAVGHTRKYRKLAKSTLVLVVFGVHYIVFVCLPHSFTGLGWEIRMHCELF 402
Db KLRTQETRGQD-MNHYKRLARSTLLIPLFGHYIVAFSPED-----AMEVOLFELALG 373

RN SEQUENCE OF 198-457 FROM N.A.
 RP TISSUE=Small intestine;
 RX MEDLINE=96206340; PubMed=8618952;
 RA Xu M., Proudman J.A., Pitts G.R., Wong E.A., Foster D.N.,
 el Halawani M.E.;
 RT "Vasoactive intestinal peptide stimulates prolactin mRNA expression
 in turkey pituitary cells: effects of dopaminergic drugs.";
 RL Proc. Soc. Exp. Biol. Med. 212:52-62(1996).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE
 CC CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in pituitary, hypothalamus, small
 CC intestine and ovarian follicles.
 CC -!- DEVELOPMENTAL STAGE: Pituitary levels are highest in
 CC nonphotostimulated and incubating birds and lower in
 CC photostimulated, laying and photorefractory birds.
 CC -!- INDUCTION: Pituitary levels decrease on VIP immunization.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announcement>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U31991; AAA99740.2; -;
 DR InterPro: IPR000832; GPCR secretin.
 DR InterPro: IPR001879; hormn_receptor.
 DR Pfam: PF000002; 7tm_2; 1.
 DR Pfam: PF02793; HRM; 1.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR SMART: SM00008; Hormr; 1.
 DR PROSITE: PS00649; G_PROTEIN_RECEP_F2.1; 1.
 DR PROSITE: PS00650; G_PROTEIN_RECEP_F2.2; 1.
 DR PROSITE: PS00227; G_PROTEIN_RECEP_F2.3; 1.
 DR PROSITE: PS0261; G_PROTEIN_RECEP_F2.4; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=99265976; PubMed=10331949;
 RA Hashimoto H., Nishino A., Shintani N., Hagiwara N., Copeland N.G.,
 RA Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
 RA Baba A.;
 RT "Genomic organization and chromosomal location of the mouse vasoactive
 intestinal polypeptide 1 (VIP1) receptor.";
 RL Genomics 58:90-93(1999).
 RN [2]
 RP SEQUENCE OF 249-398 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RX MEDLINE=96378704; PubMed=8784267;
 RA Johnson M.C., McCormack R.J., Delgado M., Martinez C., Ganea D.;
 RT "Murine T-lymphocytes express vasoactive intestinal peptide receptor
 1 (VIP-R1) mRNA.";
 RL J. Neuroimmunol. 68:109-119(1996).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
 CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL; AB022860; BAA81896.1; JOINED.
 DR EMBL; AB022848; BAA81896.1; JOINED.
 DR EMBL; AB022849; BAA81896.1; JOINED.
 DR EMBL; AB022850; BAA81896.1; JOINED.
 DR EMBL; AB022851; BAA81896.1; JOINED.
 DR EMBL; AB022852; BAA81896.1; JOINED.
 DR EMBL; AB022853; BAA81896.1; JOINED.
 DR EMBL; AB022854; BAA81896.1; JOINED.
 DR EMBL; AB022855; BAA81896.1; JOINED.
 DR EMBL; AB022856; BAA81896.1; JOINED.
 DR EMBL; AB022857; BAA81896.1; JOINED.
 DR EMBL; AB022858; BAA81896.1; JOINED.
 DR EMBL; AB022859; BAA81896.1; JOINED.
 DR EMBL; S82970; AAN86759.1; JOINED.
 DR MGD; MGI:109272; Vipr1.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; HORMR; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 459 VASOACTIVE INTESTINAL POLYPEPTIDE
 RECEPTOR 1.
 FT DOMAIN 31 143 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 144 168 1 (POTENTIAL).
 FT DOMAIN 169 175 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 176 195 2 (POTENTIAL).
 FT DOMAIN 196 217 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 218 241 3 (POTENTIAL).
 FT DOMAIN 242 255 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 256 277 4 (POTENTIAL).

FT	DOMAIN	278	294	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	318	5 (POTENTIAL).
FT	DOMAIN	319	343	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	344	363	6 (POTENTIAL).
FT	DOMAIN	364	375	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	376	395	7 (POTENTIAL).
FT	DOMAIN	396	459	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	216	286	BY SIMILARITY.
FT	CARBOHYD	58	58	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	459 AA;	52094 MW;	COC3A9AE1ADF611D CRC64;

Query Match 27.2%; Score 791.5; DB 1; Length 459;
 Best Local Similarity 36.6%; Pred. No. 3.3e-53;
 Matches 181; Conservative 81; Mismatches 145; Indels 87; Gaps 19;

QY	13	WMLGSCLLARA	---QLDSGTTIE	-----EQIVLVKAKVOCELNITQALQEGEGNCF	64
Db	11	WL----	CVLAGALACALGPASRAASPHQRCYLOMIEKQRCQCLEE	---AQLENKTTGCS	64
QY	65	PEWDGLICWDRGTGKISAVPCPPYIDFN	---HKGVAFRHCNPNGTWDFHSLMKWTWANY	122	
Db	65	KQNDNLTCNPTTPWGQVVVLDCLIFOLFSPHGINISRCTEAG	-----WSQ	112	
QY	123	SDCLRFLOP	---DISIG	-----KQECERLYVMYTVGYSGISFGLAVAILIG	167
Db	113	-----LEPGPYHACGLNDRASSMDRQOQTEFYDAVKTYGTGYTGYSLASLLVAMAILS	166		
QY	168	YERSLHCTRYNHHMLFVSEMLRATSI	FKVDKRVVHAHIGVKELESIMODDPQNSHATS	227	
Db	167	LFRKLHCTRYNHHMLFMSILRATAVFIKDM	-----ALFNNGETDRCSAS	213	
QY	228	VDKSQYIGCKIAVVMFYFLATNYTWILVGLYHNLIFVAFSDTKYLMGFLILGWGFP	287		
Db	214	-----VSKRAAVFFQYCYMANEFFWLLVEGLYHNLIFVAFSDTKYLMGFLILGWGVP	267		
QY	288	AAFVAAMAVAPATLADARWE	---LSAGDKWYQAPILAAIGLNPILFNTVTVRLATKIWE	346	
Db	268	SVFIMWTIVRIHFDPCGMDTIINSSLMWIIKPIISILVNFILICIRILVQLRCP	327		
QY	347	TNAVGHDTKQYKRLAKSTLVLVFVGVHYIVFVCLPHSFTGLGWEIRHCELFNRSFOG	406		
Db	328	PD-IGKNDSSPYSLAKSTLLILPLFGVHYVMAFFPDNFKA	---QVAMVVELVVGSGFOG	383	
QY	407	FFVSIYYCNGEVOAEVKKMSWNLS	---VDM--KETPPCGSR--CG	456	
Db	384	FWVAILYCFNGEVOAELRRKRWHLQVGLWSSKSHQHPWGGSGNGVSCSTQVSMLTRVS	443		
QY	457	-----HSTSSQSOVA	466		
Db	444	PSARRSSSFOAEVS	457		

RESULT 12
 VIPR_PIG
 ID VIPR_PIG STANDARD; PRT; 458 AA.
 AC Q28992;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1)
 DE (Pituitary adenylate cyclase activating polypeptide type II receptor)
 DE (PACAP type II receptor) (PACAP-R-2).
 GN VIPR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; U20178; AAC50106.1; -
 EMBL; U28281; AAA87556.1; -
 EMBL; U13989; AAA64949.1; -
 EMBL; AB065660; BAC05886.1; -
 F1R; JC2532; JC2532; -
 Genew; HGNC:10608; SCTR.
 MIM; 182098; -
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0015055; F:secretin receptor activity; TAS.
 GO; GO:0007586; P:digestion; TAS.
 GO; GO:0007588; P:excretion; TAS.
 GO; GO:0007186; P:g-protein coupled receptor protein signalin. . . ; TAS.
 InterPro; IPR000832; GPCR_secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm 2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G_PROTEIN_REC_F2_1; 1.
 PROSITE; PS00650; G_PROTEIN_REC_F2_2; 1.
 PROSITE; PS00651; G_PROTEIN_REC_F2_3; 1.
 PROSITE; PS00652; G_PROTEIN_REC_F2_4; 1.
 PROSITE; PS00653; G_PROTEIN_REC_F2_5; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 SIGNAL 1 22 POTENTIAL.
 CHAIN 23 440 SECRETIN RECEPTOR.
 DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 144 167 1 (POTENTIAL).
 DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 175 194 2 (POTENTIAL).
 DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 217 240 3 (POTENTIAL).
 DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 255 276 4 (POTENTIAL).
 DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 295 317 5 (POTENTIAL).
 DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 344 362 6 (POTENTIAL).
 DOMAIN 363 369 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 370 392 7 (POTENTIAL).
 DOMAIN 393 440 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CONFLICT 124 124 G -> A (IN REF. 1).
 CONFLICT 210 210 A -> P (IN REF. 2).
 CONFLICT 308 308 I -> F (IN REF. 3).
 CONFLICT 333 333 E -> Q (IN REF. 3).
 CONFLICT 377 377 G -> A (IN REF. 1).
 SEQUENCE 440 AA; 50206 MW; E22CDD0EE7C0ACC1 CRC64;
 Query Match 27.0%; Score 784; DB 1; Length 440;
 Best Local Similarity 40.5%; Pred. No. 1.2e-52;
 Matches 167; Conservative 63; Mismatches 125; Indels 57; Gaps 11;
 63 CPFEWGLCWPRGTGKISVPCPPYIDF-NHKGVAFRHCNPGTWDPMHSLNKTWAN 121
 66 CEGMDNISCSPSFGVFRVVECPFLRLMLTSRGLSFRNCTQDG-----WSE 114
 122 YSDCLRFLOPDISG-----KQFCERLYVMYTVGYSTISFGSLAVAILIIGYFR 171
 115 -----TFPRNLACGVNVDSSNEKSHYLLKLVMTYVGYSSLVMLVAILGILCAFR 169
 172 LHCTRYNHMLFVSMRLATSIFVKDRVVAHIGVKELESIMQDDPQNSIATSVSKS 231
 170 LHCTRYNHMLFVSMRLATSIFVKDRVVAHIGVKELESIMQDDPQNSIATSVSKS 231
 170 LHCTRYNHMLFVSMRLATSIFVKDRVVAHIGVKELESIMQDDPQNSIATSVSKS 231

232 QYIGCKIAVVMFYIATNYWILVEGLYHNLIFVAFSDTKYLMGFIQWGFPAFV 291
 211 HRAGCKLVWVLFQYCYIMANYMLVEGLYHNLIFVAFSDTKYLMGFIQWGFPAFV 270
 292 AAWAVARATLADARWELSA-GDIKIYQAPILALGILNFIPLNTRVRLATKINETNAV 350
 271 ALWAIARHFLVEDGVCWDINANASINWIRPVSILNFIPLNTRVRLATKINETNAV 330
 351 GHDTRAQYRKLAKSTLVLVAFGVHIVFVCLPSPHSTGLGWEIRHCELFNSFOGFFVS 410
 331 GNEV-SHYKELARSTLILPLFGIIVVAFSPED-----AMEIQLFELALSGFQLLVVA 385
 411 IYICNGEVOAEVKKWGRNLSVDWKTTPCGSRRCGSLVITVTHSTSSQ 462
 386 VLYCFLNGEVOLEVKQKQWHL-----REFPLHPVAFSPNSKASHLQSQ 432
 RESULT 14
 VIPR CARAU STANDARD; PRT; 447 AA.
 AC Q90308;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vasoactive intestinal polypeptide receptor (VIP-R) (VIP receptor).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OC NCBL_TaxID=7957;
 RN [1]
 RP MEDLINE=97190233; PubMed=9038250;
 RA Chow B.K.C.; Yuen T.T.H.; Chan K.W.;
 RT "Molecular evolution of vertebrate VIP receptors and functional
 characterization of a VIP receptor from goldfish Carassius auratus.";
 RL Gen. Comp. Endocrinol. 105:176-185(1997).
 CC Gen. Comp. Endocrinol. 105:176-185(1997).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CYCLASE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL; U56391; AAB05459.1; -
 InterPro; IPR000832; GPCR_secretin.
 InterPro; IPR001879; hormn_receptor.
 Pfam; PF00002; 7tm 2; 1.
 Pfam; PF02793; HRM; 1.
 PRINTS; PR00249; GPCRSECRETIN.
 SMART; SM00008; Hormr; 1.
 PROSITE; PS00649; G_PROTEIN_REC_F2_1; 1.
 PROSITE; PS00650; G_PROTEIN_REC_F2_2; 1.
 PROSITE; PS00651; G_PROTEIN_REC_F2_3; 1.
 PROSITE; PS00652; G_PROTEIN_REC_F2_4; 1.
 PROSITE; PS00653; G_PROTEIN_REC_F2_5; 1.
 G-protein coupled receptor; Transmembrane; Glycoprotein.
 DOMAIN 1 103 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 104 128 1 (POTENTIAL).
 DOMAIN 129 135 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 136 155 2 (POTENTIAL).
 DOMAIN 156 178 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 179 202 3 (POTENTIAL).
 DOMAIN 203 216 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 217 238 4 (POTENTIAL).
 DOMAIN 239 256 EXTRACELLULAR (POTENTIAL).

[illegible]

FT	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
QQ	459 AA; 52057 MW; 99B8957DA86698D2 CRC64;	
QQ	SEQUENCE	
Query Match	26.6%; Score 772.5; DB 1; Length 459;	
Best Local Similarity	36.8%; Pred. No. 9.2e-52;	
Matches 172; Conservative	78; Mismatches 134; Indels 83; Gaps 17;	
QY	36	EQIVLVILKAVQCELNITLAQLEGECNCFPEWDGLICWPRGTGVGISAVPCP-----PY 89
Db	38	EVLQLEIQRQOCLEB--AQLENTTGCCKWMDNLCTWPTTPRQGAUVLDCLFIQLFAP 95
QY	90	IYDNNHKGVAFRHCNPNGTWDFMHSLUNKTWANYSCLRFLOP---DISIG-----136
Db	96	IHGYN-----ISRCTEEG-----WSQ-----LEPGPYHACGLNDRASSLDE 133
QY	137	--KQECERLYVMVTVGYSISFGSLAVAILIICGYERRLHCTNTHHMLFVSEMLRATSI 194
Db	134	QQQTKFYNTVKTGTTGYLSLSLASLLVAMAILSLFRKLHCTNTHHMLFNSFILRAIV 193
QY	195	FVKDRVVHAHIGVKELESIMODDPQNSTSEATSDVSKSQYIGCKIAYVMFYFLATNYWI 254

```

Db 194 FIKDMALF-----NSGEIDHCSEAS-VGCKAAVVFQYCWMAFFWL 234
QY 255 LVEGLYLHNLIFVAFPSDTKYLWGFFILICWGFPAAFAAAMAVARATLADARCWE-LSAGD 313
Db 235 LVEGLYLYTLAVSPFSEKYPWGYILICWGVPVFIITWTVRIYFEDFGCWDTIINSS 294
QY 314 IKWIYQAPILAAIGLNFILNTRVLATKIWETNAVGHDTKQYRKLAKSTLVLVLVFG 373
Db 295 LWWIIKAPILLSLVNFVLFICIIRILVQKLRFPD-IGKNDSSPYSLAKSTLLIPLFG 353
QY 374 VHYIVFVCLPHSFTGLWEIRMHCELPFNSFOGFVSLIYCYCNGEVOAEVKKWMSRWNL 433
Db 354 IHVVMFAFFEDNPKA---QVKWVFLVWGSFOGFVVALIYCFNGEVOAELELRKRRWHL 410
QY 434 S--VDW--KRTPPCGSRR---CG---SVLTVT---HSTSSQSOVA 466
Db 411 QGVLGWSSKSQHPWGGSGNGATCSTQVSMLTRVSPSARRSSSFQAEVS 457

```

Search completed: November 21, 2003, 22:26:31
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2003, 22:23:44 ; Search time 39 Seconds
(without alignments)
3579.653 Million cell updates

Title: US-09-996-569-2

Perfect score: 2907
Sequence: 1 MAWLGA^{SL}HWG^WMLG^{SL}.....DDI^LMEK^FSPR^PME^SNP^DTEG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
SPREWEEL_23.*
1:  sp_archaea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrata.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phage.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_vertebrata.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriophage.*
17: sp_archaeophages.*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	621	4	Q8N429
2	2251.5	77.5	546	11	Q91V95
3	1677.5	57.7	575	13	Q9PWB7
4	1415.5	48.8	536	13	Q9PVD3
5	1345.5	46.3	595	6	Q9TU31
6	1324.5	45.6	591	11	Q91VW4
7	1307.5	45.0	542	13	Q9PVD2
8	962.5	33.1	964	4	Q8NH84
9	858.5	29.5	169	11	Q9R1D4
10	814	28.0	444	13	Q9VHC6
11	803.5	27.6	237	11	Q8BPM8
12	794	27.3	419	13	Q8XAV3
13	791.5	27.2	459	11	Q9J140
14	787	27.1	419	13	Q8XAV4
15	783	26.9	528	4	Q8I1V7
16	780.5	26.8	333	4	Q8NSV1
					Q8N429 homo sapien
					Q91V95 mus musculus
					Q9PWB7 brachydanio
					Q9PVD3 brachydanio
					Q9TU31 canis famil
					Q91VW4 mus musculus
					Q9PVD2 brachydanio
					Q8NH84 homo sapien
					Q9R1D4 mus musculus
					Q9VHC6 rana ridibu
					Q8BPM8 mus musculus
					Q8XAV3 fugu rubrip
					Q9J140 mus musculus
					Q8XAV4 fugu rubrip
					Q8I1V7 homo sapien
					Q8NSV1 homo sapien

17	780.5	26.8	418	13	Q9IBG2
18	713	24.4	465	13	Q73769
19	708.5	24.5	455	13	Q73769
20	702.5	24.2	438	13	Q73768
21	694	23.9	480	13	Q90Y07
22	692.5	23.8	459	11	Q8BGA4
23	685.5	23.6	465	13	Q9PTK1
24	685.5	23.6	495	13	Q90Y08
25	672.5	23.1	496	11	Q8BLT3
26	657.5	22.6	438	13	Q8AXV2
27	645.5	22.2	465	13	Q90Y09
28	645	22.2	489	13	Q8UVV4
29	644	22.2	490	13	Q8UVV5
30	636	21.9	423	6	Q9N1F8
31	635	21.8	423	6	Q9BDH9
32	633	21.8	441	6	Q9TUJ0
33	616	21.2	407	6	Q9BD10
34	610	21.0	404	6	Q9TUL1
35	604	20.8	439	11	Q9W099
36	594	20.4	478	11	Q924D5
37	594	20.4	495	11	Q924D6
38	593	20.4	485	11	Q8K0B5
39	592	20.4	492	13	Q9PUK1
40	593.5	20.3	532	11	Q924D7
41	589	20.3	533	11	Q8CAB0
42	582	20.0	374	6	Q8W0E0
43	567	19.5	402	6	Q8W0Q9
44	566.5	19.5	589	6	Q9GMD1
45	557	19.2	414	13	Q8AWA1

ALIGNMENTS

RESULT 1

Q8N429	PRELIMINARY;	PRT;	621 AA.
AD	Q8N429;		
IC	Q8N429;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, last annotation update)		
DE	Parathyroid hormone receptor 2 (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Eute-		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homi-		
OX	NCBI_TaxId=9606;		
RN	[1]_TaxId=9606;		
RP	SEQUENCE FROM N.A.		
RA	TISSUE=Brain;		
RA	Strausberg R.;		
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC036811; AAH36811.1;		
DR	InterPro; IPR000832; GPCR_secretin.		
DR	InterPro; IPR001879; hormn_receptor.		
DR	Pfam; PF00002; 7tm_2; 1.		
DR	Pfam; PF02793; HRM; 1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	SMART; SM00008; HormR; 1.		
DR	PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.		
DR	PROSITE; PS50227; G_PROTEIN_RECP_F2_3; 1.		
DR	PROSITE; PS50261; G_PROTEIN_RECP_F2_4; 1.		
DR	Receptor.		
KW	NON_TER		
FT	SEQUENCE 621 AA; 69299 MW; 8B0A5A84889436D2 CRC64;		
SQ			

	Query Match	90.6%	Score 2635;	DB 4;	Length 621;
	Best Local Similarity	91.4%;	Pred. No. 1.6e-234;		
	Matches 500;	Conservative	6;	Mismatches 29;	Indels 12; Gaps 3;
Qy	1	MAWLGLSHVWGWMIGSCLLARAQ	LDSDGTITIEEQI	VLVLKAKVQCELNITAAQ	QEGE 60
db	72	MAGLGLSHVWGWMIGSCLLARAQ	LDSDGTITIEEQI	VLVLKAKVQCELNITAAQ	QEGE 131


```

QY 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
DB 132 GNCFFPMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 191
QY 121 NYSDCRLFLQPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
DB 192 NYSDCRLFLQPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 251
QY 181 MHLFVSFMLRATSIFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDSKSYIGCKIAV 240
DB 252 MHLFVSFMLRATSIFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDSKSYIGCKIAV 311
QY 241 VMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFLIIGWGPFAAFVAWAVARAT 300
DB 312 VMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFLIIGWGPFAAFVAWAVARAT 371
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 360
DB 372 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 431
QY 361 LAKSTVLVLVFGVHVIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCYCNGEV 420
DB 432 LAKSTVLVLVFGVHVIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCYCNGEV 491
QY 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 477
DB 492 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCL---SLAK 551
QY 478 LPRSPADSLTATSLYLAWSGVTSQRTASHTLS---TRSNKEDSGRQDDILMEKPSRPME 534
DB 552 IASRQPDSD---HITLPGVWSNSEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 605
QY 535 SNPDTEG 541
DB 606 SNPDTEG 612

RESULT 2
Q91V95
ID Q91V95 PRELIMINARY; PRT; 546 AA.
AC Q91V95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone receptor.
GN PTHR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, and ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.B., Sikela J.M.;
RT "High-throughput Sequence Identification of Gene Coding Variants
RT within Alcohol-Related QTLs.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
EX MEDLINE=22354883; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF332078; AAK56106.1; -.
DR EMBL; AF332077; AAK56105.1; -.
DR EMBL; AK045576; BAC32420.1; -.
DR MGD; MGI:2180917; Pthr2.
DR InterPro; IPR000832; GPCR_secretin.

```

```

DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR02793; HRM; 1.
DR SMART; SM00249; GPCRSECRETIN.
DR SMART; SM00008; Horm8; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
DR Receptor.
SQ SEQUENCE 546 AA; 61908 MW; 628051EF181A1DF3 CRC64;

Query Match 77.5%; Score 2251.5; DB 11; Length 546;
Best Local Similarity 78.3%; Pred. No. 3.4e-199;
Matches 426; Conservatve 34; Mismatches 75; Indels 9; Gaps 4;

QY 1 MAWLGAASLVGWMLGSCLLARAOQSDGTTIBEQIVLVKAKVQCCLNITAIQOE 60
DB 1 MAWLFTFYICWLLISSLCLLVRAQSDGTTIBEQIVLVKAKVQCCLNITAIQOE 60
QY 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
DB 61 GNCFFPMDGLICWPRGTGKISAVPCPPYIDFNHKGVAFRHCNPNCTWDFMHSLNKTWA 120
QY 121 NYSDCRLFLQPDISIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 180
DB 121 NYSDC--FLQPDINIGKQEFCEFLRYVMYTVGYSISFGSLAVAILIIGYFRLHCTRYIH 178
QY 181 MHLFVSFMLRATSIFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDSKSYIGCKIAV 240
DB 179 LHLFVSFMLRATSIFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDSKSYIGCKIAV 238
QY 241 VMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFLIIGWGPFAAFVAWAVARAT 300
DB 239 VMFIYFLATNYWILVEGLYLNLIIFVAFPSDTKYLWGFLIIGWGPFAAFVAWAVARAT 298
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 360
DB 299 LADARCWELSGAD--RWIYQAPILAAIGLNFILFNTVRLVATKIWETNAVGHDTKQYRK 357
QY 361 LAKSTVLVLVFGVHVIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCYCNGEV 420
DB 358 LAKSTVLVLVFGVHVIVFVCLPHSFTGLGWEIRMHCELFNFSFGFFVSIYCYCNGEV 417
QY 421 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCLSLAKLPR 480
DB 418 QAEVKQWGRWNLSDWKRTPPCGSRRCGSLVTTVTHSTSSQSOVAHAHAWCLSLAKLPR 477
QY 481 SPA---DSLTSYLAWSGVTSQRTASHTLSRKNKEDSGRQDDILMEKPSRPME 537
DB 478 NACRQIDSHVTLPGYVWSSEQDCQTHSPPEBET---KEGHRHQDDSPWMBESSRPVAF 534
QY 538 DTEG 541
DB 535 DTEG 538

RESULT 3
Q9PWB7
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Parathyroid hormone type-2 receptor.
GN PTHR2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;

```

RESULT	4
ID	Q9PVD3
ID	PRELIMINARY;
AC	PRT; 536 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	Parathyroid hormone receptor PTHR.
GN	PTHr1.
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query, Match	48.88;	Score	1418.5;	DB	13;	Length	536;
Best Local Similarity	57.88;	Fried. Mat.	2.8e-122;				
Matches	269;	Conservative	80;	Mismatches	107;	Indels	9;
Gaps	6;						
QY	4	LGASLHV--WGMWMLASCL--LARAQDSDSGTITTBEEQVLVLVKAKVQCELNITAAQLOQE	60				
Db	1	MGATLIVRTLGLFCGTLLSFVYGLVDADVLTKEEQVLLFNAKKCCERALKSKHKTSE	60				
QY	61	GNCPPEWDGLICWPRGTGVGKISAVPCPPIYDFNKHGVAFRHCPNPGTWDPMHSLNKTWA	120				
Db	61	GSCLPEWDGLICWPEGVPGKMWSTSCPEYIYDFNKHGHAYRRCDLNGTWELASHNNTWA	120				
QY	121	NYSDCLAFLQDISIGKQECERLIVMYVTWGSISFGSLAVALITIGYFRRLHCTRVYIH	180				
Db	121	NYSECAFPFHYNQNERVFDRLIYIVGVYSIGSLWATVILGYFRRLHCTRVYIH	180				
QY	181	MHLFVSMLRATSIFFVKDRVWHAHIGVKELESILMQDDPQNSIBATSVDSQYTGCKIAV	240				
Db	181	MHLFLSFLMLRAISIFVKDVLVYSGSALQMERITV--EDLKSITEAPPANKQTQIGCVAV	239				
QY	241	VNFYFYLATNYITVLVEGLYLNLIIFVAPPSDTKYLWGFILMGCFPAFVAANAVARAT	300				
Db	240	TLFYFYLATNYITVLVEGLYLHSLIIPMTFPSDKYLWGFILIGWGPAMPFTIIVASVRAT	299				
QY	301	LADARCWELSGADIKWIIYQAPILAAITGLNFILPLNTVRVLATKIWTETNAVGHDTKQYRK	360				
Db	300	LADTECDWLSAGNLKWIVQIPIITAVVNFLLFLNIIRVLATKURETNAGRCDTQQYRK	359				
QY	361	LAKSTLVILVIVFGHYIVVPCVLPHS--FTGLGWIEIRMHCBELFNSPQGFVSIIVCYCNQE	419				
Db	360	LLKSTVLVMPFPGHYIVVFNAMPEYIVTEVSGVLWQIQMHYEMLEFNSVQGFVAILIYFCNGE	419				
QY	420	VOAEYKKMWKRWNLVSDVMWKTPPPCGSR--RCGSVL--TTVTHSTS	460				
Db	420	VOAEIKKAWNRRTIALDFKSKARCSGNTSYGYGPMVSHTSYIVNTVA	464				

RESULT 5	
ID Q9TU31	PRELIMINARY; PRT; 595 AA.
Q9TU31	
AC Q9TU31:	
DT 01-MAY-2000	(TRENBLrel. 13, Created)
DT 01-MAY-2000	(TRENBLrel. 13, Last sequence update)
DT 01-OCT-2001	(TRENBLrel. 18, Last annotation update)
DE	Parathyroid hormone receptor-1.

GN PTH1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN NCBI_TaxID=9615;
 FN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
 RT "Molecular cloning and functional characterization of the canine
 parathyroid hormone receptor-1 (PTHr).";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF167095; AAD5938.1; -
 DR HSP; Q03431; 1BL1.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;
 Query Match 46.3%; Score 1345.5; DB 6; Length 595;
 Best Local Similarity 46.5%; Pred. No. 1.8e-115;
 Matches 281; Conservative 90; Mismatches 154; Indels 79; Gaps 11;
 QY 4 LGASLHVGMMLGSCLL--ARRAQLSDSGTITIEQIVLVKAKVQCELNITAIQIQ--- 57
 DB 1 MGAVRIAPGLALLCCPVLSSAVALVADDDVMTKEEQIFLLHRAQAQCCKRLKEVLQPEA 60
 QY 58 -----EKG-----CPPEWGLICWPR 75
 DB 61 DIMESDKWASASTSGPKKKEKASKGLYPSEEDKEVPTSGRHGRPCLPENWHILCWPL 120
 QY 76 GTVGKISAVPCPPYIYDFNHKGAVFRHCNPNGTWDFMHSLNKTWANYSDCLRFQPDISI 135
 DB 121 GAPGEVAVPCPDYIYDFNHKGAVFRCDRNGSWELVPGHRTWANYSECVKELTNETR- 179
 QY 136 GKQFCERLYVMYTVGSISSGLAVALLIIGYPRRLHCTRNHYHMLFVSPMLRATSI 195
 DB 180 -REVFDRLGMIYTVGYSVSLASTVAVLLAYFRRLHCTRNHYHMLFVSPMLRAVSIF 238
 QY 196 VKDRVWHAHIGVKELES-----IMQDDPQNSIEATSDKSYIGCKIAVVMFYFLA 248
 DB 239 VKDAVLISGATLDEAERLIEELRAIAQAPPPPTAAA-----GYACRVAVTFYFLA 292
 QY 249 TNYTWILVEGLYLNHLIFVAPFSDTKYLMGFIIGWGFPAAFVAWAVARATLADARWE 308
 DB 293 TNYTWILVEGLYLNHLIFVAPFSDTKYLMGFIIGWGFPAAFVAWAVARATLADARWE 352
 QY 309 LSAGDIKIWIYQAPILAAIGLNFLPLNTVRVATKIWTETNAVGHDTKQYRKLAKSTLVL 368
 DB 353 LSSGNKMIIOVPIIASLVLMFLINLVIRVATKURETNAGRCDTQQYRKLAKSTLVL 412
 QY 369 VLVFVGHYIVFVCLPHS--FTGLGWIRMHCELFNSFGFPVSIYCYNGEVAQAEVKKM 427
 DB 413 MFLFGVHYIVFMATPYTEVSGTLNQVQMHYEMLFNSFGFPVSIYCYNGEVAQAEIKKS 472
 QY 428 WSRNMLSDVWRTPPPGRRRCGSLVTTVTHSTSSQSQVAHAHAWCLSLAKLPRSPADSLT 487
 DB 473 WSRWTLALDFKRAKSGSSSY-SYCPMVSHTSVTVNVPRAGLGLPLSPRLIPAAAAATTA 531
 QY 488 ATSLYLSANGSVTQSTASHTL-----STRSKED-----SGQRDDILMEKPSRWES 535
 DB 532 TTNHPPPIPGHT--KPGAPTLPATPPATAAPKDDGFLNGSCSGLDESASAPERPALQ 589
 QY 536 NPDT 539
 ;

DB 590 EWET 593
 RESULT 6
 Q91WV4
 ID Q91WV4 PRELIMINARY; PRT; 591 AA.
 AC Q91WV4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Parathyroid hormone receptor.
 GN PTHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013446; AAH13446.1; -
 DR MGD; MGI:97801; Pthr.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63E5BAFEED CRC64;
 Query Match 45.6%; Score 1324.5; DB 11; Length 591;
 Best Local Similarity 50.5%; Pred. No. 1.5e-117; Indels 61; Gaps 7;
 Matches 258; Conservative 75; Mismatches 117;
 QY 22 ARAQLSDSGTITIEQIVLVKAKVQCE-----LNITAIQIQEGEN----- 62
 DB 22 AVALVDADDVTFKEQIFLLHRAQAQCCKLKEVLHTAANIMESDKGWTASTSGKPKKE 81
 QY 63 -----CPPEWGLICWPR-----CPPEWGLICWPR----- 156
 DB 82 KAPGKFYPESKENKDVPTGSRGRPCLPENWDINVCWPLGAPGEVAVPCPDYIYDFNHK 141
 QY 97 GVAFPHCPNGTWDFMHSLNKTWANYSDCLRFQPDISIYQYKISAVPCPPYIYDFNHK 156
 DB 142 GHAYRCDRNGSWELVPGHRTWANYSECLAFMTNETR--REVFDRLGMIYTVGYSNL 199
 QY 157 GSLAVALLIIGYPRRLHCTRNHYHMLFVSPMLRATSIYFVDRVWHAHIGVKELES--- 213
 DB 200 ASLTAVALLAYFRRLHCTRNHYHMLFVSPMLRAASIFVDAVLYSGFTLDEAERLTEE 259
 QY 214 ----IMQDDPQNSIEATSDKSYIGCKIAVVMFYFLATNYWILVEGLYLNHLIFVAF 269
 DB 260 ELHIIAQVPPPPAAAAVG-----YACRVAVTFYFLATNYWILVEGLYLNHLIFVAF 314
 QY 270 FSDTKYLMGFIIGWGFPAAFVAWAVARATLADARWEISAGDIKIWIYQAPILAAIGLN 329
 DB 315 FSEKYLWGFIFGNGLPFAVFAVWVAVRATLANTGCDLSSGHKKKIIQVPIIASLVLN 374
 QY 330 FILFNTVRVATKIWTETNAVGHDTKQYRKLAKSTLVLVIFGVHYIVFVCLPHS-PTG 388
 DB 375 FILFINIRVATKURETNAGRCDTQQYRKLAKSTLVLVIFGVHYIVFVCLPHS-PTG 434
 QY 389 LGWEIRMHCELFNSFGFPVSIYCYNGEVAQAEVKKWSRNMLSDVWRTPPPGRRRC 448
 DB 435 TLWQIQMHYEMLFNSFGFPVSIYCYNGEVAQAEVKKWSRNMLSDVWRTPPPGRRRC 494
 QY 449 GSVLTVTHTSSSQSQVAHAHAWCLSLAKLP 479


```

Db 572 WILVEGLYHSLIFMAFFSEKKVLWGFTVFGWGLPAFVAVVVSVRATLANTGVQPPDA- 630
QY 313 DIKWIYQAPILAAIGLNFILNTRVRLATKIWETNAVGHDTKQY----- 358
Db 631 -----APSLFQ--LNFILFINIVRLATKIRETNAGRCDDTQQQVRSGLALTLYLPRWP 681
QY 359 RKLAKSTLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSF----- 404
Db 682 RKLKSTLVLMPLFGVHYIVFMATPYTEVSGTLMQVMHYEMLFNSFQVRSAGPLAEGG 741
QY 405 -----QGFVSIICYNGEVOAEVKQKSWRNLSVDWKTPPCGSRRCG- 449
Db 742 RGSQGRPDRSPSSQGFVAILIYFCFNGEVOAEIKKSWRNLTALDFKRSKSSSY 801
QY 450 SVLTIVTHSTSSQSOVAAHAWCLSLAKLPRSPADSLTATSL-YLAMSGVTSKRT-ASHT 507
Db 802 GPVSHTSVTVNVRVLG-----LPLSPRLPTATNGHPQLPGHAKGTPALET 852
QY 508 LSTRS-----NKDSQGRDDILMEKPSRPMESNPDTEG 541
Db 853 LETPPAMAAPKDDGFLNGSCGLDERASGPERPPALLOQEWETVISGDHLEG 905

RESULT 9
Q9R1D4
ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OS Parathyroid hormone type-2 receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones."
RL J. Biol. Chem. 274:23035-23042 (1999).
DR EMBL; AF132083; AAD51909.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR PRINTS; PR00249; GPCRSSECRETIN.
DR PROSITE; PS00002; 7tm_2; 1.
DR PFAM; PF00002; 7tm_2; 1.
FT NON_TER 1 1
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231F1C69EA CRC64;

Query Match 29.5%; Score 858.5; DB 11; Length 169;
Best Local Similarity 92.9%; Pred. No. 3.5e-71;
Matches 158; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 250 NYWILVEGLYHNLIIIVAPFSDTKYLWGFTLIGWGPFAAFVAAVARATLADARCWEL 309
Db 1 NYWILVEGLYHNLIIIVSFSDTKYLWGFTSIGWGPFAFVAVAVARATLADTRCWEL 60
QY 310 SAGDIKWTQAPILAAIIGLNFILNTRVRLATKIWETNAVGHDTKQYKRLAKSTLVLV 369
Db 61 SAGD-RWTYQAPILAAIIGLNFILNTRVRLATKIWETNAVGHDMRKQYKRLAKSTLVLV 119
QY 370 LVFGVHYIVFVCLPHSTGLGWEIRMHCELFNSFQGFVSIICYNGE 419
Db 120 LVFGVHYIVFVCLPHSTGLGWEIRMHCELFNSFQGFVSIICYNGE 169

RESULT 10

```

```

Q9VHC6
ID Q9VHC6 PRELIMINARY; PRT; 444 AA.
AC Q9VHC6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Vasoactive intestinal peptide/pituitary adenylate cyclase activating
DE polypeptide receptor.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=99165178; PubMed=10067855;
RA Alexandre D., Anouar Y., Jegou S., Fournier A., Vaudry H.;
RT "A cloned frog vasoactive intestinal polypeptide/pituitary adenylate
RT cyclase-activating polypeptide receptor exhibits pharmacological and
RT tissue distribution characteristics of both VPAC1 and VPAC2 receptors
RT in mammals."
RL Endocrinology 140:1285-1293 (1999).
DR EMBL; AF100644; AAD03602.1; -.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR PFAM; PF00002; 7tm_2; 1.
DR PFAM; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_5; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_6; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_7; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_8; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_9; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_10; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_11; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_12; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_13; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_14; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_15; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_16; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_17; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_18; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_19; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_20; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_21; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_22; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_23; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_24; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_25; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_26; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_27; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_28; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_29; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_30; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_31; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_32; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_33; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_34; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_35; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_36; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_37; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_38; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_39; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_40; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_41; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_42; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_43; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_44; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_45; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_46; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_47; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_48; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_49; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_50; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_51; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_52; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_53; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_54; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_55; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_56; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_57; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_58; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_59; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_60; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_61; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_62; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_63; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_64; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_65; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_66; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_67; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_68; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_69; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_70; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_71; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_72; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_73; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_74; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_75; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_76; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_77; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_78; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_79; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_80; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_81; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_82; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_83; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_84; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_85; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_86; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_87; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_88; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_89; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_90; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_91; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_92; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_93; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_94; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_95; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_96; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_97; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_98; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_99; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_100; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_101; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_102; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_103; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_104; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_105; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_106; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_107; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_108; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_109; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_110; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_111; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_112; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_113; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_114; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_115; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_116; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_117; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_118; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_119; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_120; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_121; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_122; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_123; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_124; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_125; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_126; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_127; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_128; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_129; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_130; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_131; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_132; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_133; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_134; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_135; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_136; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_137; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_138; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_139; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_140; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_141; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_142; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_143; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_144; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_145; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_146; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_147; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_148; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_149; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_150; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_151; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_152; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_153; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_154; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_155; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_156; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_157; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_158; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_159; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_160; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_161; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_162; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_163; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_164; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_165; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_166; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_167; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_168; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_169; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_170; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_171; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_172; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_173; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_174; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_175; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_176; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_177; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_178; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_179; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_180; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_181; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_182; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_183; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_184; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_185; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_186; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_187; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_188; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_189; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_190; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_191; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_192; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_193; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_194; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_195; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_196; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_197; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_198; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_199; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_200; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_201; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_202; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_203; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_204; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_205; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_206; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_207; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_208; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_209; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_210; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_211; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_212; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_213; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_214; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_215; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_216; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_217; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_218; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_219; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_220; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_221; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_222; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_223; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_224; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_225; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_226; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_227; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_228; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_229; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_230; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_231; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_232; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_233; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_234; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_235; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_236; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_237; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_238; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_239; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_240; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_241; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_242; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_243; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_244; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_245; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_246; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_247; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_248; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_249; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_250; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_251; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_252; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_253; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_254; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_255; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_256; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_257; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_258; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_259; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_260; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_261; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_262; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_263; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_264; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_265; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_266; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_267; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_268; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_269; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_270; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_271; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_272; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_273; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_274; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_275; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_276; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_277; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_278; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_279; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_280; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_281; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_282; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_283; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_284; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_285; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_286; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_287; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_288; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_289; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_290; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_291; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_292; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_293; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_294; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_295; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_296; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_297; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_298; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_299; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_300; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_301; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_302; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_303; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_304; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_305; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_306; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_307; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_308; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_309; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_310; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_311; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_312; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_313; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_314; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_315; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_316; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_317; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_318; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_319; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_320; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_321; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_322; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_323; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_324; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_325; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_326; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_327; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_328; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_329; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_330; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_331; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_332; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_333; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_334; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_335; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_336; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_337; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_338; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_339; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_340; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_341; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_342; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_343; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_344; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_345; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_346; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_347; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_348; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_349; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_350; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_351; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_352; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_353; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_354; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_355; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_356; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_357; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_358; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_359; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_360; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_361; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_362; 
```


[illegible]

Search completed: November 21, 2003, 22:27:24
Job time : 41 secs